

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:46:20 ; Search time 10.16 Seconds
(without alignments)
57.740 Million cell updates/sec

Title: US-09-647-457-2
Perfect score: 16
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 100059 seqs, 36664827 residues

Word size: 0

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database: SWISSProt_39:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	7	43.8	335	1 MPBL_HUMAN	P22712 homo sapien
2	7	43.8	395	1 ENO_ALMT	P42897 alligator m
3	7	43.8	433	1 ENOA_ANAPL	P19140 anas platyr
4	7	43.8	433	1 ENOA_BOVIN	O9XSJ4 bos taurus
5	7	43.8	433	1 ENOA_CHICK	P51913 gallus gall
6	7	43.8	433	1 ENOA_HUMAN	P06733 homo sapien
7	7	43.8	433	1 ENOA_MOUSE	P17182 mus musculu
8	7	43.8	433	1 ENOA_RAT	P04764 rattus norv
9	7	43.8	433	1 ENOA_CHICK	P07322 gallus gall
10	7	43.8	433	1 ENOA_HUMAN	P13929 homo sapien
11	7	43.8	433	1 ENOA_MOUSE	P21550 mus musculu
12	7	43.8	433	1 ENOA_RABIT	P25704 coryctolagus
13	7	43.8	433	1 ENOA_RAT	P15429 rattus norv
14	7	43.8	433	1 ENOA_HUMAN	P09104 homo sapien
15	7	43.8	433	1 ENOG_MOUSE	P17183 mus musculu
16	7	43.8	433	1 ENOG_RAT	P07323 rattus norv
17	7	43.8	433	1 ENO_HONGA	P56252 homarus gam
18	7	43.8	433	1 ENO_XENLA	P08734 xenopus lae
19	7	43.8	434	1 ENO_LODPE	O02654 loligo peal
20	7	43.8	434	1 ENO_SCHUA	P33676 schistosoma
21	7	43.8	434	1 ENO_SCHUA	O21877 schistosoma
22	7	43.8	458	1 ENOL_HUMAN	O05524 homo sapien
23	7	43.8	142	1 HBA3_PLEMA	P11896 pleurodeles
24	6	37.5	231	1 YE93_MENJA	O58888 methanococc
25	6	37.5	433	1 RTCL_DICDI	O15746 dictyosteli
26	6	31.2	88	1 FLIO_HELPY	O25964 helicobacte
27	5	31.2	94	1 FER_RHOPL	P74931 treponema p
28	5	31.2	97	1 FER_RHOPL	O92365 schizosacch
29	5	31.2	99	1 R36A_SCHPO	O94658 schizosacch
30	5	31.2	99	1 R36B_SCHPO	O95252 sus scrofa
31	5	31.2	101	1 B3AR_PIG	O95252 sus scrofa
32	5	31.2	106	1 FER6_RHOCA	P80306 rhododactyl
33	5	31.2	120	1 NU3C_MAIZE	P19044 zea mays (m

34	5	31.2	120	1 NU3C_ORYSA	P12126 oryza sativ
35	5	31.2	120	1 NU3C_WHEAT	P26303 triticum ae
36	5	31.2	134	1 RL27_PVRST	O02984 pyrobolus
37	5	31.2	152	1 YF47_STVY3	P74662 synecocyst
38	5	31.2	157	1 YSA4_ECOLI	P36256 escherichia
39	5	31.2	169	1 LSHB_HORSE	P08751 equus cabal
40	5	31.2	172	1 NU6M_CYPCA	P24982 cyprinus ca
41	5	31.2	173	1 NU6M_AETPY	P43191 aethia pygm
42	5	31.2	173	1 NU6M_CARAU	O78689 carassius a
43	5	31.2	173	1 NU6M_FRACR	P43201 fratercula
44	5	31.2	173	1 NU6M_LATCH	O03175 latimeria c
45	5	31.2	173	1 NU6M_PTYAL	P43203 ptychoramph

ALIGNMENTS

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RESULT 1
MPBL_HUMAN STANDARD; PRT; 335 AA.
ID MPBL_HUMAN
AC P22712:
DT 01-AUG-1991 (Rel. 19, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE C-MYC PROMOTER-BINDING PROTEIN (MPB-1) (MBP-1).
GN MPB1 OR MBP1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=91172204; PubMed=2005901;
RA Ray R., Miller D.M.;
RT "Cloning and characterization of a human c-myc promoter-binding
RT Protein."
RL Mol. Cell. Biol. 11:2154-2161(1991).
CC 1. FUNCTION: BINDS TO THE C-MYC PROMOTER REGION OF THE C-MYC GENE
CC AND IS THOUGHT TO REPRESS TRANSCRIPTION.
CC 2. SUBCELLULAR LOCATION: NUCLEAR (PROBABLE).
CC 3. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 4. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 5. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 6. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 7. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 8. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 9. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 10. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 11. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 12. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 13. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 14. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 15. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 16. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 17. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 18. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 19. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 20. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 21. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 22. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 23. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 24. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 25. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 26. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 27. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 28. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 29. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 30. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 31. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 32. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC 33. SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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Query Match 43.8%; Score 7; DB 1; Length 335;
Best Local Similarity 100.0%; Pred. No. 1.5;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
Db 285 LVVGLCT 291

RESULT 2

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END_ALMT
ID ENO_ALMT STANDARD; PRT; 395 AA.
AC P42897;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Crocodylia; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=94195794; PubMed=8146164;
RA Medline=8-B.
RT "Molecular evidence for the origin of birds".
RL Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H2O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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CC -----
DR EMBL: L28078; AA53671.1; -.
DR HSSP: P56252; LPDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium.
FT METAL 136 136 BY SIMILARITY.
FT ACT_SITE 1 1
FT METAL 223 223 MAGNESIUM (BY SIMILARITY).
FT METAL 271 271 MAGNESIUM (BY SIMILARITY).
FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
FT NON_TER 395 395
SQ SEQUENCE 395 AA; 42884 MW; BA3E91228E9110B5 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 395;
Best Local Similarity 100.0%; Pred. No. 1.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
ID ENO_ALMT STANDARD; PRT; 433 AA.
AC P19140;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DE 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (TAU-DEHYDRATASE).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;

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RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89079778; PubMed=2462567;
RA Wislow G.J., Lieberman T., Williams L.A., Stapel S.O., de Jong W.W., Horwitz J., Plaforsky J.,
RT "tau-cristallin/alpha-enolase-one gene encodes both an enzyme and a lens structural protein."
RL J. Cell Biol. 107:2729-2736(1988).
CC -1- FUNCTION: BOTH AN ENZYME AND A LENS STRUCTURAL PROTEIN.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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CC -----
DR EMBL: M20749; AA49218.1; -.
DR EMBL: X14195; CAA32409.1; -.
DR PIR: A32132; A32132.
DR HSSP: P56252; LPDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium; Eye lens protein.
FT INIT_MET 0 0
FT ACT_SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 433 AA; 47108 MW; 1AED78B08A6E8AD CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
ID ENO_BOVIN STANDARD; PRT; 433 AA.
AC O9X574;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DE 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOENOLPYRUVATE DEHYDRATASE).
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovidae; Bovidae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chapman K.L., Newman B., Hillaby M.C., Freemont A.J., Grant M.E.,
RA Boot-Handford R., Wallis G.A.;

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RT "Alpha enolase is upregulated in proliferative chondrocytes in the
RT epiphyseal growth plate and in human osteoarthritic tissue.";
RT Submitted (May-1999) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC EMBL: AF149256; AAD33073.1; -.
CC DR HSSP: P56252; 1PDZ.
CC DR InterPro: IPR000941; Enolase.
CC DR Pfam: PF00113; enolase.1.
CC DR PRINTS: PR00148; ENOLASE.
CC KW Lyase; Glycolysis; Magnesium; Multigene family.
CC FT INIT_MET 0
CC FT ACT_SITE 157 157 BY SIMILARITY.
CC FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 433 AA; 47145 MW; B004E965C46F2E0C CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
Db 383 LVGLCT 389

RESULT 5
ENOA_CHICK STANDARD: PRT; 433 AA.
ID ENOA_CHICK
AC P51913;
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (PHOSPHOPYRUVATE HYDRATASE).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX SPRAIN-WHITE LEGHORN; TISSUE=Kidney;
RX MEDLINE=95355305; PubMed=7629021;
RA Tanaka M., Maeda K., Nakashima K.;
RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent
RT tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence
RT analysis.";
RT J. Biochem. 117:554-559(1995).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING

CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC EMBL: D37900; BAA07132.1; -.
CC DR HSSP: P56252; 1PDZ.
CC DR InterPro: IPR000941; Enolase.
CC DR Pfam: PF00113; enolase.1.
CC DR PRINTS: PR00148; ENOLASE.
CC DR ProDom: PD000902; Enolase.1.
CC DR PROSITE: PS00164; ENOLASE; 1.
CC KW Lyase; Glycolysis; Magnesium; Multigene family.
CC FT INIT_MET 0
CC FT ACT_SITE 157 157 BY SIMILARITY.
CC FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 433 AA; 47173 MW; 93AD6B0A7AD99910 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
Db 383 LVGLCT 389

RESULT 6
ENOA_HUMAN STANDARD: PRT; 433 AA.
ID ENOA_HUMAN
AC P06733; Q16704; Q9UM55;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
DE NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
DE ENO1 OR ENO1L1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86313654; PubMed=3529090;
RX Gallongo A., Feo S., Moore R., Croce C.M., Showne L.C.;
RT "Molecular cloning and nucleotide sequence of a full-length cDNA for
RT human alpha enolase.";
RT Proc. Natl. Acad. Sci. U.S.A. 83:6741-6745(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90323004; PubMed=2373081;
RX Gallongo A., Oliva D., Cali L., Barba G., Barbieri G., Feo S.;
RT "Structure of the human gene for alpha-enolase.";
RT Eur. J. Biochem. 190:567-573(1990).
RN [3]
RP SEQUENCE FROM N.A.
RX TISSUE=Endometrium;
RX MEDLINE=96422099; PubMed=8824716;
RX Walter M., Leidenberger F.A., Scheppe K.W., Berg H., Northmann W.;
RT "Autoreactive epitopes within the human alpha-enolase and their
RT recognition by sera from patients with endometriosis.";

RL J. Autoimmun. 8:937-945(1995).
 RN [4]
 RP SEQUENCE OF 165-433 FROM N.A.
 RA MEDLINE=98317532; PubMed=9653645;
 RX Onyango P., Lubkova B., Gardellin P., Kurzbauer R., Weith A.;
 RT "Molecular cloning and expression analysis of five novel genes in
 RL chromosome 1p36.";
 RN Genomics 50:187-198(1998).
 RN [5]
 RP SEQUENCE OF 269-280 AND 306-320.
 RA MEDLINE=95307697; PubMed=7787969;
 RX Mohamed R.M., Hamdan M.Y., Maki A., Al-Katib A.;
 RT "Induced expression of alpha-enolase in differentiated diffuse large
 RL cell lymphoma.";
 RN Enzyme Protein 48:37-44(1995).
 RN [6]
 RP SEQUENCE OF 1-8.
 RC TISSUE-Colon carcinoma;
 RA MEDLINE=97295306; PubMed=9150948;
 RX Ji H., Reid G.E., Moritz R.L., Eddes J.S., Burgess A.W., Simpson R.J.;
 RT "A two-dimensional gel database of human colon carcinoma proteins.";
 RL Electrophoresis 18:605-613(1997).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COPACITOR: MAGNESIUM IS REQUIRED FOR CATALYSTS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: M14328; AAA52387.1; -
 DR EMBL: M14388; CAA34360.1; -
 DR EMBL: X16289; CAA34360.1; JOINED.
 DR EMBL: X16290; CAA34360.1; JOINED.
 DR EMBL: X84907; CAA59331.1; -
 DR EMBL: U88968; AAC39935.1; -
 DR PIR: A29170; A29170.
 DR PIR: S11696; S11696.
 DR HSP: P56252; 1PDY.
 DR Aarhus/Ghent-2DPAGE; 1325; IEF.
 DR Aarhus/Ghent-2DPAGE; 5406; NEPHGE.
 DR MIM: 172430; -
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE; 1.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Multigene family.
 FT INT MET 0
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
 FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
 FT CONFLICT 251 251 F -> S (IN REF. 3).
 SQ SEQUENCE 433 AA; 47037 MW; B2028684C33140B5 CRC64;

QY 1 LVGLCT 7
 ID 111111
 Db 383 LVGLCT 389
 RESULT 7
 ENOA_MOUSE STANDARD; PRT; 433 AA.
 AC P17182; O9DCY7;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 20-AUG-2001 (Rel. 40, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
 DE NEURAL ENOLASE) (NNE).
 GN ENOI OR ENO-1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=90301487; PubMed=2362815;
 RA Kaghad M., Dumont X., Chalon P., Lelias J.M., Lamande N., Lucas M.,
 RA Lazar M., Caput D.;
 RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from
 RL mouse brain.";
 RN Nucleic Acids Res. 18:3638-3638(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6J; TISSUE=Kidney;
 RX MEDLINE=21085660; PubMed=11217851;
 RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
 RA Areakawa T., Hara A., Fukunishi Y., Konno H., Aachi J., Fukuda S.,
 RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamana K.I.,
 RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
 RA Kadota K., Matsuda H.A., Ashburner M., Batilov S., Casavant T.,
 RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochava H.,
 RA Kiehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
 RA Schiraldi L.M., Staudli F., Suzuki R., Tomita M., Wagner L., Washio T.,
 RA Sakai K., Orido T., Futuno M., Kono H., Baldarelli R., Barish G.,
 RA Blake J., Borrelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
 RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
 RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamita M., Lee N.H.,
 RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Momberees P.,
 RA Norcone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
 RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata T., Storch K.-F.,
 RA Suzuki H., Toyooka K., Wang K.H., Weitz C., Whitaker C., Wilming L.,
 RA Wysshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohsaki S.,
 RA Hayashizaki Y.;
 RT "Functional annotation of a full-length mouse cDNA collection.";
 RL Nature 409:685-690(2001)
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COPACITOR: MAGNESIUM IS REQUIRED FOR CATALYSTS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC or send an email to license@isb-sib.ch).
 CC -----

Query Match 43.8%; Score 7; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 1.9;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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CC -----
CC EMBL: X52379; CAA36605.1; -
CC EMBL: AK002336; BAB22021.1; -
CC PIR: S10246; S10246.
CC HSSP: P56252; LPDY.
CC SWISS-2DPAGE: P17187; MOUSE.
CC MGD: MGI:95393; ENOL.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC KX Lyase: Glycolysis; Magnesium; Multigene family.
CC FT INT_MET 0
CC FT ACT_SITE 157 157 BY SIMILARITY.
CC FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC FT CONFLICT 358 358 L -> P (IN REF. 1).
CC SQ SEQUENCE 433 AA; 47009 MW; C90082CBA8290EB6 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
Db 383 LVVGLCT 389

RESULT 8
ENOA_RAT
ID ENOA_RAT STANDARD; PRT; 433 AA.
AC P04764;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
DE NEUTRAL ENOLASE) (NNE).
DE ENOI OR ENO-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=85242108; PubMed=2989793;
RA Sakimura K., Kushiya E., Ohinata M., Takahashi Y.;
RT "Molecular cloning and the nucleotide sequence of cDNA to mRNA for
RT non-neutonal enolase (alpha alpha enolase) of rat brain and liver.",
RT Nucleic Acids Res. 13:4365-4378(1985).
RL [2]
RN SEQUENCE FROM N.A.
RA Takahashi Y.;
RT Submitted (JAN-1986) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X02610; CAA26456.1; -
CC PIR: A23126; A23126.
CC HSSP: P56252; LPDY.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC KX Lyase: Glycolysis; Magnesium; Multigene family.
CC FT INT_MET 0
CC FT ACT_SITE 157 157 BY SIMILARITY.
CC FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 433 AA; 46984 MW; F1A25F010C276ETC CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
Db 383 LVVGLCT 389

RESULT 9
ENOB_CHICK
ID ENOB_CHICK STANDARD; PRT; 433 AA.
AC P07322;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (PHOSPHOPYRUVATE HYDRATASE).
DE Gallus gallus (Chicken).
OS Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauilia; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae.
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Muscle;
RX MEDLINE=9535305; PubMed=7629021;
RA Tanaka M., Maeda K., Nakashima K.;
RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent
RT tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence
RT analysis.",
RT J. Biochem. 117:554-559(1995).
RL [2]
RN SEQUENCE.
RX MEDLINE=87075592; PubMed=3539098;
RA Russell G.A., Dunbar B., Fothergill-Limmore L.A.;
RT "The complete amino acid sequence of chicken skeletal-muscle
RT enolase.",
RL Biochem. J. 236:115-126(1986).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC EMBL: D37901, BAA07133.1, -

DR PIR: A23850, A23850.

DR HSSP: P56252, 1PDY.

DR InterPro: IPR000941, Enolase.

DR Pfam: PF00113, enolase.1.

DR PRINTS: PR00148, ENOLASE.

DR ProDom: PD000902, ENOLASE.1.

DR PROSITE: PS00164, ENOLASE.1.

KW Lyase; Glycolysis; Magnesium; Multigene family; Acetylation.

FT INIT-MET 0

FT MOD-RES 1

FT ACT-SITE 157 157

FT METAL 244 244

FT METAL 292 292

FT METAL 317 317

FT CONFLICT 16 16

FT CONFLICT 48 48

FT CONFLICT 93 93

FT CONFLICT 118 119

FT CONFLICT 208 208

FT CONFLICT 257 257

FT CONFLICT 265 266

FT CONFLICT 308 308

FT CONFLICT 322 322

FT CONFLICT 330 330

FT CONFLICT 342 342

FT CONFLICT 393 394

SO SEQUENCE 433 AA; 47065 MW; 9BC2B5FB910C254 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYGLCT 7

Db 383 LVYGLCT 389

RESULT 10

ENOB HUMAN STANDARD; PRT; 433 AA.

AC P13929; 01-JAN-1990 (Rel. 13, Created)

DT 01-OCT-1993 (Rel. 27, Last sequence update)

DT 20-AUG-2001 (Rel. 40, Last annotation update)

DE BETA ENOLASE (EC 4.2.1.11) (2-PROSPHO-D-GLYCERATE HYDRO-LYASE)

DE (SKLEFAL MUSCLE ENOLASE) (MSE).

GN ENO3.

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

OX NCBI_Taxid=9606;

RM [1]

RP SEQUENCE FROM N.A.

RX MEDLINE-90067857; PubMed-2567223;

RA Peshavaria M., Hinks L.J., Day I.N.M.;

RT "Structure of human muscle (beta) enolase mRNA and protein deduced from a genomic clone."

RL Nucleic Acids Res. 17:8862-8862(1989).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE-91222137; PubMed-1840492;

RA Peshavaria M., Day I.N.M.;

RT "Molecular structure of the human muscle-specific enolase gene (ENO3)."

RL Biochem. J. 275:427-433(1991).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE-90245587; PubMed-2336366;

RA Call L., Feo S., Oliva D., Giallongo A.;

RT "Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE)."

RL Nucleic Acids Res. 18:1893-1893(1990).

RN [4]

RP SEQUENCE FROM N.A.

RX MEDLINE-93292497; PubMed-8513787;

RA Giallongo A., Ventrella S., Oliva D., Barbieri G., Rubino P., Feo S.;

RT "Structural features of the human gene for muscle-specific enolase. Differential splicing in the 5'-untranslated sequence generates two forms of mRNA."

RL Eur. J. Biochem. 214:367-374(1993).

CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.

CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER.

CC -1- PATHWAY: GLYCOLYSIS.

CC -1- SUBUNIT: HOMODIMER.

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.

CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS FOUND ONLY IN NERVOUS TISSUE.

CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC EMBL: X16504; CAA34513.1; -

DR EMBL: X51957; CAA36216.1; -

DR EMBL: X55976; CAA39446.1; -

DR EMBL: X56832; CAA40163.1; -

DR PIR: S15933; S15933.

DR PIR: S06756; S06756.

DR PIR: S14759; S14759.

DR PIR: S31650; S31650.

DR PIR: S33330; S33330.

DR HSSP: P56252; 1PDY.

DR MIM: 131370; -

DR InterPro: IPR000941, Enolase.

DR Pfam: PF00113, enolase.1.

DR PRINTS: PR00148, ENOLASE.

DR ProDom: PD000902, ENOLASE.1.

DR PROSITE: PS00164, ENOLASE.1.

KW Lyase; Glycolysis; Magnesium; Multigene family.

FT INIT-MET 0

FT ACT-SITE 157 157

FT METAL 244 244

FT METAL 292 292

FT METAL 317 317

FT CONFLICT 84 84

FT CONFLICT 161 161

SO SEQUENCE 433 AA; 46855 MW; 5F726D743DEB82F CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYGLCT 7

Db 383 LVYGLCT 389

RESULT 11

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ENOB_MOUSE
ID ENOB_MOUSE STANDARD: PRT: 433 AA.
AC P2150;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
GN ENO3 OR ENO-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/C; TISSUE=Liver;
RA Lamande N., Brosset S., Keller A., Lucas M., Lazar M.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RA MEDLINE=92290133; PubMed=1339335;
RA Peterson C.A., Cho M., Rastinejad F., Blau H.M.;
RA "Beta-enolase is a marker of human myoblast heterogeneity prior to
RA differentiation";
RL Dev. Biol. 151:626-629(1992).
RN [3]
RP SEQUENCE OF 58-433 FROM N.A.
RA MEDLINE=89282789; PubMed=2734297;
RA Lamande N., Mazo A.M., Lucas M., Montarras D., Pinsel C., Gros F.,
RA Legault-Demare L., Lazar M.;
RA "Murine muscle-specific enolase: cDNA cloning, sequence, and
RA developmental expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4445-4449(1989).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2O).
CC -1- COPACITOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X61600; CAA43797.1; -
CC EMBL: X62667; CAA44540.1; -
CC EMBL: M20745; AAA37554.1; -
CC EMBL: X57747; CAA40913.1; -
CC PIR: S17109; NOKSB.
CC PIR: A33921; A33921.
CC PIR: S29675; S29675.
CC HSSP: P56252; 1PDY.
CC SWISS-2DPAGE: P21550; MOUSE.
CC MGD: MGI:95395; P15503; MOUSE.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC PRODOM: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT_MET 0
FT ACT_SITE 157 157 BY SIMILARITY.

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FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 233 234 AG -> NA (IN REF. 3).
SQ SEQUENCE 433 AA; 40893 MW; B31B5763382D3FA8 CMC64;

Query Match
Best Local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7 43.8%; Score 7; DB 1; Length 433;
||||||| Pred. No. 1.9;
Db 383 LVVGLCT 389

RESULT 12
ENOB_RABBIT STANDARD: PRT: 433 AA.
AC P25704; O9N0N6;
DT 01-MAY-1992 (Rel. 22, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
GN ENO3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=9113295; PubMed=2275753;
RA Chin C.C.O.;
RA "The primary structure of rabbit muscle enolase.";
RL J. Protein Chem. 9:427-432(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Zheng S.-X.;
RA "The cDNA cloning of rabbit muscle-specific enolase gene, site
RA directed mutagenesis (R417L) of the gene, expression of the wild-type
RA and mutant genes in Escherichia coli.";
RL Thesis (1995), Concordia University, Montreal / Quebec, Canada.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2O).
CC -1- COPACITOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF260259; AAF71925.1; -
CC PIR: A37210; A37210.
CC HSSP: P56252; 1PDY.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC PRODOM: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.

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Lyase; Glycolysis; Magnesium; Multigene family.
 KW INIT_MET 0
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
 FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
 FT CONFLICT 253 253 N -> D (IN REF. 1).
 FT CONFLICT 296 296 N -> D (IN REF. 1).
 SQ SEQUENCE 433 AA; 46859 MW; 063A4005443C0403 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVGLICT 7
 Db 383 LVGLICT 389

RESULT 13

ENOB_RAT STANDARD; PRT; 433 AA.
 AC P15429;

DT 01-APR-1990 (Rel. 14, Created)
 DT 01-APR-1990 (Rel. 14, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 DE (SKELETAL MUSCLE ENOLASE).
 GN ENO3 OR ENO-3.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=MISTAR;
 RX MEDLINE=89121113; PubMed=2914621;
 RA Oshima Y., Mitsui H., Takayama Y., Kushiya E., Sakimura K.,
 RA Takahashi Y.,
 RT "CDNA cloning and nucleotide sequence of rat muscle-specific enolase
 (beta beta enolase).";
 RL FEBS Lett. 242:425-430(1989).
 RN [2]

RP SEQUENCE OF 1-27 FROM N.A.
 RX MEDLINE=91099531; PubMed=2269373;
 RA Sakimura K., Kushiya E., Oshima-ichimura Y., Mitsui H.,
 RA Takahashi Y.,
 RT "Structure and expression of rat muscle-specific enolase gene";
 RL FEBS Lett. 277:78-82(1990).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE - PHOSPHOENOLPYRUVATE
 + H₂O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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 or send an email to license@isb-sib.ch).

DR EMBL: Y00979; CA68788.1; -
 DR EMBL: X57774; CAA40920.1; -

DR PIR: S02072; S02072.
 DR HSSP: P56252; IPDY.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Multigene family.
 FT INIT_MET 0
 FT ACT_SITE 157 157 BY SIMILARITY.
 FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
 FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
 FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 433 AA; 46829 MW; 4C2CBDB12DBA536D CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
 Best Local Similarity 100.0%; Pred. No. 1.9;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVGLICT 7
 Db 383 LVGLICT 389

RESULT 14

ENOG_HUMAN STANDARD; PRT; 433 AA.
 AC P09104;

DT 01-MAR-1989 (Rel. 10, Created)
 DT 01-MAR-1989 (Rel. 10, Last sequence update)
 DT 20-AUG-2001 (Rel. 40, Last annotation update)
 DE GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 DE (NEURAL ENOLASE) (NSE).
 GN ENO2.
 OS Homo sapiens (Human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_TaxID=9606;
 RN [1]
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
 RC TISSUE=Retina;
 RX MEDLINE=89091176; PubMed=3208766;
 RA McAliese S.M., Dunbar B., Fothergill J., Hinks L., Day I.N.M.;
 RT "Complete amino acid sequence of the neurone-specific gamma isozyme
 of enolase (NSE) from human brain and comparison with the
 non-neuronal alpha form (NSE).";
 RL Eur. J. Biochem. 178:413-417(1988).
 RN [2]

RP SEQUENCE FROM N.A.
 RX MEDLINE=9006764; PubMed=2792767;
 RA Oliva D., Barba G., Barbieri G., Giallongo A., Feo S.;
 RT "Cloning, expression and sequence homologies of cDNA for human gamma
 enolase";
 RL Gene 79:355-360(1989).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX TISSUE=Brain;
 RA van Oberghehen E., Kamholz J., Bishop J.G. III, Zomzely-Neurath C.,
 RA Lazzerini R.A.;
 RT "Human gamma enolase: isolation of a cDNA clone and expression in
 normal and tumor tissues of human origin";
 RL J. Neurosci. Res. 19:450-456(1988).
 RN [4]

RP SEQUENCE FROM N.A.
 RX TISSUE=Hematopoietic;
 RX MEDLINE=91257823; PubMed=2045099;
 RA Oliva D., Cali L., Feo S., Giallongo A.;
 RT "Complete structure of the human gene encoding neuron-specific
 enolase";
 RL Genomics 10:157-165(1991).
 RN [5]

```

RP SEQUENCE FROM N.A.
RX MEDLINE=96303695; PubMed=8723724;
RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E.,
RT Spanos S., Mailey T., Gibbs R.A.;
RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
RL genes at human chromosome 12p13."
RL Genome Res. 6:314-326(1996).
RN [6]
RP SEQUENCE OF 424-433 FROM N.A.
RX MEDLINE=88005129; PubMed=3653393;
RA Day I.N.M., Allsopp M.T.E.P., Moore D.C.M., Thompson R.J.;
RT "Sequence conservation in the 3'-untranslated regions of neurone-
RT specific enolase, lymphokine and protooncogene mRNAs."
RL FEBS Lett. 223:139-143(1987).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X13120; CAA31512.1; -
CC EMBL: M22349; AAB59554.1; -
CC EMBL: M36768; AAA52388.1; ALT_INIT.
CC EMBL: X51956; CAA36215.1; -
CC EMBL: U47924; AAB51320.1; -
CC EMBL: X14327; CAA32505.1; -
CC PIR: J00060; NOHUG.
CC PIR: S02077; S02077.
CC PIR: S02616; S02616.
CC HSSP: P56252; 1PDY.
CC MIM: 131360; -
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lysase; Glycolysis; Magnesium; Multigene family; Polymorphism.
CC INT_MET 0
CC ACT_SITE 157
CC METAL 244
CC METAL 292
CC METAL 317
CC METAL 317
CC VARIANT 263
CC VARIANT 394
CC VARIANT 394
CC CONFLICT 3
CC CONFLICT 27
CC CONFLICT 126
CC CONFLICT 126
CC CONFLICT 239
CC CONFLICT 239
CC SEQUENCE 433 AA; 47154 MW; 0F01A8A5FF9152A1 CRC64;

Query Match 43.8%; Score 7; DB 1; Length 433;
Best local Similarity 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVGLCT 7.

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DB 383 LVVGLCT 389
RESULT 15
ID ENOG_MOUSE STANDARD; PRT; 433 AA.
AC P17183;
DT 01-AUG-1990 (Rel. 15, Created)
DT 01-AUG-1990 (Rel. 15, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (NEURAL ENOLASE) (NSE).
GN ENO2 OR ENO-2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90301487; PubMed=2362815;
RA Kaged M., Dumont X., Chalon P., Lelias J.M., Lemande N., Lucas M.,
RA Lazar M., Caput D.;
RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from
RT mouse brain."
RL Nucleic Acids Res. 18:3638-3638(1990).
RN [2]
RP SEQUENCE FROM N.A.
RA Ansari-Lari M.A., Oeljen J.C., Schwartz S., Zhang Z., Muzny D.M.,
RA Lu J., Gorrell J.H., Chinnault A.C., Belmont J.W., Miller W.,
RA Gibbs R.A.;
RL Submitted (AUG-1997) to the EMBL/Genbank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X52380; CAA36606.1; -
CC EMBL: AC002397; AAC36002.1; -
CC PIR: S10247; S10247.
CC HSSP: P56252; 1PDY.
CC MGD: MGI:95394; Eno2.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; Enolase; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lysase; Glycolysis; Magnesium; Multigene family.
CC INT_MET 0
CC ACT_SITE 157
CC METAL 244
CC METAL 292
CC METAL 317
CC SEQUENCE 433 AA; 47165 MW; B7281132E637D43E CRC64;

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Query Match 43.88; Score 7; DB 1; Length 433;
Best Local Similarly 100.0%; Pred. No. 1.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGICCT 7
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DB 383 LVVGICCT 389

Search completed: May 8, 2002, 11:47:58
Job time: 98 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:45:09 ; Search time 23.85 Seconds
(without alignments)
49.693 Million cell updates/sec

Title: US-09-647-457-2

Sequence: 1 LVYGLCTCQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0, Gapext 60.0

Searched: 522463 seqs, 74073290 residues

Word size: 0

Total number of hits satisfying chosen parameters: 522463

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database:

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- 2: /SIDS8/gcgdata/geneseq/geneseq/AA1981.DAT:*
- 3: /SIDS8/gcgdata/geneseq/geneseq/AA1982.DAT:*
- 4: /SIDS8/gcgdata/geneseq/geneseq/AA1983.DAT:*
- 5: /SIDS8/gcgdata/geneseq/geneseq/AA1984.DAT:*
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- 13: /SIDS8/gcgdata/geneseq/geneseq/AA1992.DAT:*
- 14: /SIDS8/gcgdata/geneseq/geneseq/AA1993.DAT:*
- 15: /SIDS8/gcgdata/geneseq/geneseq/AA1994.DAT:*
- 16: /SIDS8/gcgdata/geneseq/geneseq/AA1995.DAT:*
- 17: /SIDS8/gcgdata/geneseq/geneseq/AA1996.DAT:*
- 18: /SIDS8/gcgdata/geneseq/geneseq/AA1997.DAT:*
- 19: /SIDS8/gcgdata/geneseq/geneseq/AA1998.DAT:*
- 20: /SIDS8/gcgdata/geneseq/geneseq/AA1999.DAT:*
- 21: /SIDS8/gcgdata/geneseq/geneseq/AA2000.DAT:*
- 22: /SIDS8/gcgdata/geneseq/geneseq/AA2001.DAT:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	16	100.0	16	AAV43191	Schizophrenic deri
2	8	50.0	16	AAV43204	Schizophrenic deri
3	8	50.0	17	AAV43197	Schizophrenic deri
4	8	50.0	17	AAV43198	Schizophrenic deri
5	7	43.8	15	AAV43203	Schizophrenic deri
6	7	43.8	16	AAV43202	Schizophrenic deri
7	7	43.8	17	AAV43196	Schizophrenic deri
8	7	43.8	18	AAV43195	Schizophrenic deri
9	7	43.8	19	AAV43194	Schizophrenic deri
10	7	43.8	20	AAV43193	Schizophrenic deri
11	7	43.8	20	AAV43199	Schizophrenic deri

13	7	43.8	28	AAV43192	Schizophrenic deri
14	7	43.8	21	AAV43191	Breast and ovarian
15	7	43.8	21	AAV43191	Human ORFX OGF1828
16	7	43.8	18	AAV43191	Enolase protein.
17	6	37.5	19	AAV43191	Alpha Enolase. Ho
18	6	37.5	16	AAV43200	Schizophrenic deri
19	6	37.5	22	AAV43199	Human EST encoded
20	6	37.5	22	AAV43199	Moraxella catarrha
21	6	37.5	22	AAV43199	C glutamicum prote
22	6	37.5	22	AAV43199	Corynebacterium q1
23	6	37.5	22	AAV43199	Human protein kina
24	5	31.2	7	AAV43199	Human microtubule
25	5	31.2	9	AAV43199	Uroplakin tumour a
26	5	31.2	12	AAV43199	Penicillin V amido
27	5	31.2	12	AAV43199	Schizophrenic deri
28	5	31.2	14	AAV43199	Cladosporium herba
29	5	31.2	16	AAV43199	Fibroblast growth
30	5	31.2	18	AAV43199	Antimicrobial cati
31	5	31.2	20	AAV43199	Bactolysin - antim
32	5	31.2	20	AAV43199	Cationic antimicro
33	5	31.2	21	AAV43199	Hepatitis GB virus
34	5	31.2	21	AAV43199	Staphylococcus aur
35	5	31.2	21	AAV43199	Human secreted pro
36	5	31.2	21	AAV43199	Human 5' EST secre
37	5	31.2	21	AAV43199	E21, monoclonal an
38	5	31.2	21	AAV43199	Human endometrium
39	5	31.2	21	AAV43199	Arabidopsis thalia
40	5	31.2	21	AAV43199	Plant SDF encoded
41	5	31.2	21	AAV43199	Secreted protein e
42	5	31.2	21	AAV43199	Amino acid sequenc
43	5	31.2	21	AAV43199	Human endometrium
44	5	31.2	21	AAV43199	Arabidopsis thalia
45	5	31.2	22	AAV43199	Human colon cancer

ALIGNMENTS

RESULT 1

AAV43191

ID AAV43191 standard; peptide; 16 AA.

XX

AC AAV43191;

XX

DT 11-JAN-2000 (first entry)

XX

DE Schizophrenic derived antibody binding epitope #1.

XX

KW Schizophrenic derived antibody; binding epitope; schizophrenia;

KW platelet-associated antibody; diagnosis.

OS

OS Synthetic.

XX

PN W09951725-A2.

XX

PD 14-OCT-1999.

XX

PF 30-MAR-1999; 99WO-IL00190.

XX

PR 02-APR-1998; 98IL-0123925.

XX

PA (YEDA) YEDA RES & DEV CO LTD.

XX

PI Shinitzky M, Deckmann M;

XX

DR WPI: 1999-611037/52.

XX

PT New peptides useful for diagnosis of schizophrenia -

XX

PS Claim.2; Page 21; 37pp; English.

XX

CC This sequence is a peptide of the invention, which binds antibodies found

CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

XX Sequence 16 AA;

Query Match

Best Local Similarity 100.0%; Score 16; DB 20; Length 16;

Matches 16; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16
 |||||
 DB 1 LVVGLCTCQIKTGPAC 16

RESULT 2

AAV43204 standard; peptide; 16 AA.

XX AAV43204;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #14.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KM platelet-associated antibody; diagnosis.

XX Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

PS Claim 4; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

XX Sequence 16 AA;

Query Match

Best Local Similarity 50.0%; Score 8; DB 20; Length 16;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QIKTGPAC 16
 |||||

DB 9 qiktgpac 16

RESULT 3

AAV43197 standard; peptide; 17 AA.

XX AAV43197;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #7.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KM platelet-associated antibody; diagnosis.

XX Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.

XX Sequence 17 AA;

Query Match

Best Local Similarity 50.0%; Score 8; DB 20; Length 17;

Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 9 QIKTGPAC 16
 |||||
 DB 9 qiktgpac 16

RESULT 4

AAV43198 standard; peptide; 17 AA.

XX AAV43198;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #8.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KM platelet-associated antibody; diagnosis.

XX Synthetic.

PN WO9951725-A2.
XX
PD 14-OCT-1999.
XX
PF 30-MAR-1999; 99WO-IL00190.
XX
PR 02-APR-1998; 98IL-0123925.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Shinitzky M, Deckmann M;
XX
DR WPI; 1999-611037/52.
XX
PT New peptides useful for diagnosis of schizophrenia -
XX
PS Claim 3; Page 21; 37pp; English.
XX
CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 17 AA;

Query Match 50.0%; Score 8; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.06;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 9 QIKTGPAC 16
| | | | | | | |
Db 9 qiktgpac 16

RESULT 5
AAV43203
ID AAV43203 standard; peptide; 15 AA.
XX
AC AAV43203;
XX
DT 11-JAN-2000 (first entry)
XX
DE Schizophrenic derived antibody binding epitope #13.
XX
KW Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.
XX
OS Synthetic.
XX
PN WO9951725-A2.
XX
PD 14-OCT-1999.
XX
PF 30-MAR-1999; 99WO-IL00190.
XX
PR 02-APR-1998; 98IL-0123925.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Shinitzky M, Deckmann M;
XX
DR WPI; 1999-611037/52.
XX
PT New peptides useful for diagnosis of schizophrenia -
XX
PS Claim 4; Page 21; 37pp; English.
XX

CC This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 15 AA;

Query Match 43.8%; Score 7; DB 20; Length 15;
Best Local Similarity 100.0%; Pred. No. 0.57;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
| | | | | | |
Db 1 lvvgldct 7

RESULT 6
AAV43202
ID AAV43202 standard; peptide; 16 AA.
XX
AC AAV43202;
XX
DT 11-JAN-2000 (first entry)
XX
DE Schizophrenic derived antibody binding epitope #12.
XX
KW Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.
XX
OS Synthetic.
XX
PN WO9951725-A2.
XX
PD 14-OCT-1999.
XX
PF 30-MAR-1999; 99WO-IL00190.
XX
PR 02-APR-1998; 98IL-0123925.
XX
PA (YEDA) YEDA RES & DEV CO LTD.
XX
PI Shinitzky M, Deckmann M;
XX
DR WPI; 1999-611037/52.
XX
PT New peptides useful for diagnosis of schizophrenia -
XX
PS Claim 4; Page 21; 37pp; English.
XX
PN This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
SQ Sequence 16 AA;

Query Match 43.8%; Score 7; DB 20; Length 16;
Best Local Similarity 100.0%; Pred. No. 0.6;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7

Db 1 LVVGLCT 7

RESULT 7

AAV43196
ID AAV43196 standard; peptide: 17 AA.

XX AAV43196;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #6.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
in elevated levels in body fluids of schizophrenic patients. The peptide
is useful in an assay for the diagnosis of schizophrenia, by binding the
peptide to a platelet-containing fraction of blood, or a fraction
containing platelet-associated antibodies (PAA) shed from the platelets,
or preferably whole blood. The new peptides are able to differentiate
between plasma samples from schizophrenic and non-schizophrenic patients,
and can do so without having to first isolate the platelet-associated
antibodies (PAA) fraction.

CC Sequence 17 AA;

SQ

Query Match 43.8%; Score 7; DB 20; Length 17;
Best Local Similarity 100.0%; Pred. No. 0.63;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7

Db 1 LVVGLCT 7

RESULT 8

AAV43195
ID AAV43195 standard; peptide: 18 AA.

XX AAV43195;

AC 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #5.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

XX WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
in elevated levels in body fluids of schizophrenic patients. The peptide
is useful in an assay for the diagnosis of schizophrenia, by binding the
peptide to a platelet-containing fraction of blood, or a fraction
containing platelet-associated antibodies (PAA) shed from the platelets,
or preferably whole blood. The new peptides are able to differentiate
between plasma samples from schizophrenic and non-schizophrenic patients,
and can do so without having to first isolate the platelet-associated
antibodies (PAA) fraction.

CC Sequence 18 AA;

SQ

Query Match 43.8%; Score 7; DB 20; Length 18;
Best Local Similarity 100.0%; Pred. No. 0.66;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7

Db 2 LVVGLCT 8

RESULT 9

AAV43194
ID AAV43194 standard; peptide: 19 AA.

XX AAV43194;

AC 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #4.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 XX
 SQ Sequence 19 AA;

Query Match 43.8%; Score 7; DB 20; Length 19;
 Best Local Similarity 100.0%; Pred. No. 0.69;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 3 lvvglt 9

RESULT 10
 AAY43193
 ID AAY43193 standard; peptide; 20 AA.

XX AAY43193;

XX 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #3.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

XX Synthetic.

XX WO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL00190.

XX 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

XX Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 XX
 SQ Sequence 20 AA;

Query Match 43.8%; Score 7; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 4 lvvglt 10

RESULT 11
 AAY43199
 ID AAY43199 standard; peptide; 20 AA.

XX AAY43199;

XX 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #9.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

XX Synthetic.

XX WO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL00190.

XX 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

XX Claim 4; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 XX
 SQ Sequence 20 AA;

Query Match 43.8%; Score 7; DB 20; Length 20;
 Best Local Similarity 100.0%; Pred. No. 0.72;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 12 lvvglt 18

RESULT 12
 AAY43192
 ID AAY43192 standard; peptide; 28 AA.

XX AAY43192;

XX 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #2.

XX Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.

XX

OS Synthetic.
XX
XX WO9951725-A2.
XX
XX 14-OCT-1999.
XX
XX 30-MAR-1999; 99WO-IL00190.
XX
XX 02-APR-1998; 98IL-0123925.
XX
XX (YEDA) YEDA RES & DEV CO LTD.
XX
XX
XX Shinitzky M, Deckmann M;
XX
XX WPI; 1999-611037/52.
XX
XX New peptides useful for diagnosis of schizophrenia -
PS
XX Claim 3; Page 21; 37pp; English.
XX
XX This sequence is a peptide of the invention, which binds antibodies found
CC in elevated levels in body fluids of schizophrenic patients. The peptide
CC is useful in an assay for the diagnosis of schizophrenia, by binding the
CC peptide to a platelet-containing fraction of blood, or a fraction
CC containing platelet-associated antibodies (PAA) shed from the platelets,
CC or preferably whole blood. The new peptides are able to differentiate
CC between plasma samples from schizophrenic and non-schizophrenic patients,
CC and can do so without having to first isolate the platelet-associated
CC antibodies (PAA) fraction.
XX
XX Sequence 28 AA;
SQ

Query Match 43.8%; Score 7; DB 20; Length 28;
Best Local Similarity 100.0%; Pred. No. 0.95;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
| | | | | | |
Db 12 LVVGLCT 18

RESULT 13
AAB58877
ID AAB58877 standard; protein; 218 AA.
XX
AC AAB58877;
XX
DT 27-MAR-2001 (first entry)
XX
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 585.

XX
KW Human; breast cancer; ovarian cancer; cytostatic; immunosuppressive;
KW neurotropic; neuroprotective; antiviral; antifungal; hepatotropic;
KW antidiabetic; antiparasitic; antitumor; vulnary; anticonvulsant;
KW antibacterial; antifungal; antiparasitic; candidant; immune disorder;
KW Addison's disease; allergy; autoimmune haemolytic anaemia;
KW autoimmune thyroiditis; diabetes mellitus; Crohn's disease;
KW multiple sclerosis; rheumatoid arthritis; ulcerative colitis;
KW cardiovascular disorder; wound healing; neurological disease.
XX
OS Homo sapiens.
XX
XX WO20005173-A1.
XX
XX 21-SEP-2000.
XX
XX 08-MAR-2000; 2000WO-US05881.
XX
XX 12-MAR-1999; 99US-0124270.
XX
XX (HUMA-) HUMAN GENOME SCI INC.
XX
XX

PI Rosen CA, Ruben SM;
XX
XX WPI; 2000-611515/58.
XX
XX N-PSDB; AAF21780.
XX
XX New human breast and ovarian cancer associated gene sequences and the
PT polypeptides encoded by these genes, useful in the prevention,
PT treatment and diagnosis of cancer, immune disorders, cardiovascular
PT disorders and neurological diseases -
XX
XX Claim 11; Page 1022-1023; 1299pp; English.
XX
XX

XX
XX Sequences AAF21614 - AAF22031 represent DNA sequences encoding human
CC proteins AAB58711 - AAB59128. The DNA and protein sequences are
CC associated with breast and ovarian cancer. Included in the invention are
CC sequences AAF22032 - AAF22040 and AAB59129 which are used in the
CC isolation and characterisation of the DNA and protein sequences of the
CC invention. The breast and ovarian cancer associated DNA, protein, agonist
CC or antagonist sequences exhibit cytostatic; immunosuppressive;
CC neurotropic; neuroprotective; antiviral; antifungal; hepatotropic;
CC antidiabetic; antiparasitic; antitumor; vulnary; anticonvulsant;
CC antibacterial; antifungal; antiparasitic and candidant activity. The
CC polynucleotide and protein sequences are used in the diagnosis of cancer,
CC particularly breast and ovarian cancer. The nucleic acid sequences,
CC proteins, agonists and antagonists may also be used in the diagnosis,
CC prevention and treatment of immune disorders e.g. Addison's disease,
CC allergies, autoimmune haemolytic anaemia, autoimmune thyroiditis,
CC diabetes mellitus, Crohn's disease, multiple sclerosis, rheumatoid
CC arthritis and ulcerative colitis; cardiovascular disorders such as
CC myocardial ischaemia; wound healing; neurological diseases such as
CC cerebral anoxia and epilepsy; and infectious diseases.
XX
XX Sequence 218 AA;
SQ

Query Match 43.8%; Score 7; DB 21; Length 218;
Best Local Similarity 100.0%; Pred. No. 5.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 LVVGLCT 7
| | | | | | |
Db 43 LVVGLCT 49

RESULT 14
AAB42064
ID AAB42064 standard; protein; 429 AA.
XX
AC AAB42064;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human ORF1828 polypeptide sequence SEQ ID NO:3656.

XX
KW Human; open reading frame; ORF; detection; cytostatic; hepatotropic;
KW vulnary; antiparasitic; antiparasitoid; neurotropic; neuroprotective;
KW anticonvulsant; osteopathic; antiarthritis; immunosuppressant; candidant;
KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
KW antiviral; antibacterial; antifungal; antineumatic; antithyroid;
KW antianemic; gene therapy; cancer; proliferative disorder; hypertension;
KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
KW cholesterol ester storage; systemic lupus erythematosus; infection;
KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
KW bone damage; cartilage damage; antinflammatory disease; coagulation;
KW thrombosis; contraceptive.
XX
OS Homo sapiens.
XX
XX WO200058473-A2.
XX
XX
XX

PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 XX
 DR WPI; 2000-602362/57.
 DR N-PSDB; AAC76273.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 11; Page 2810-2811; 5507pp; English.
 XX
 CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytostatic; hepatotropic; vulnary;
 CC antipariatic; antiparkinsonian; nootropic; neuroprotective;
 CC osteoparatic; anticonvulsant; antiallthritic; immunosuppressant;
 CC immunostimulant; cardiac; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antinflammatory; antibacterial; antiviral; antifungal; antineumatic;
 CC antihypertoid; and antianemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy.
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,
 CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
 CC allergies, aplastic anemia, burns, wounds, bone and cartilage damage,
 CC nocturnal haemoglobinuria, antinflammatory disease; to enhance
 CC coagulation; to inhibit thrombosis; and as a contraceptive.
 CC
 XX
 SQ Sequence 429 AA;
 OY 1 LVVGICT 7
 DB 379 LVVGICT 385

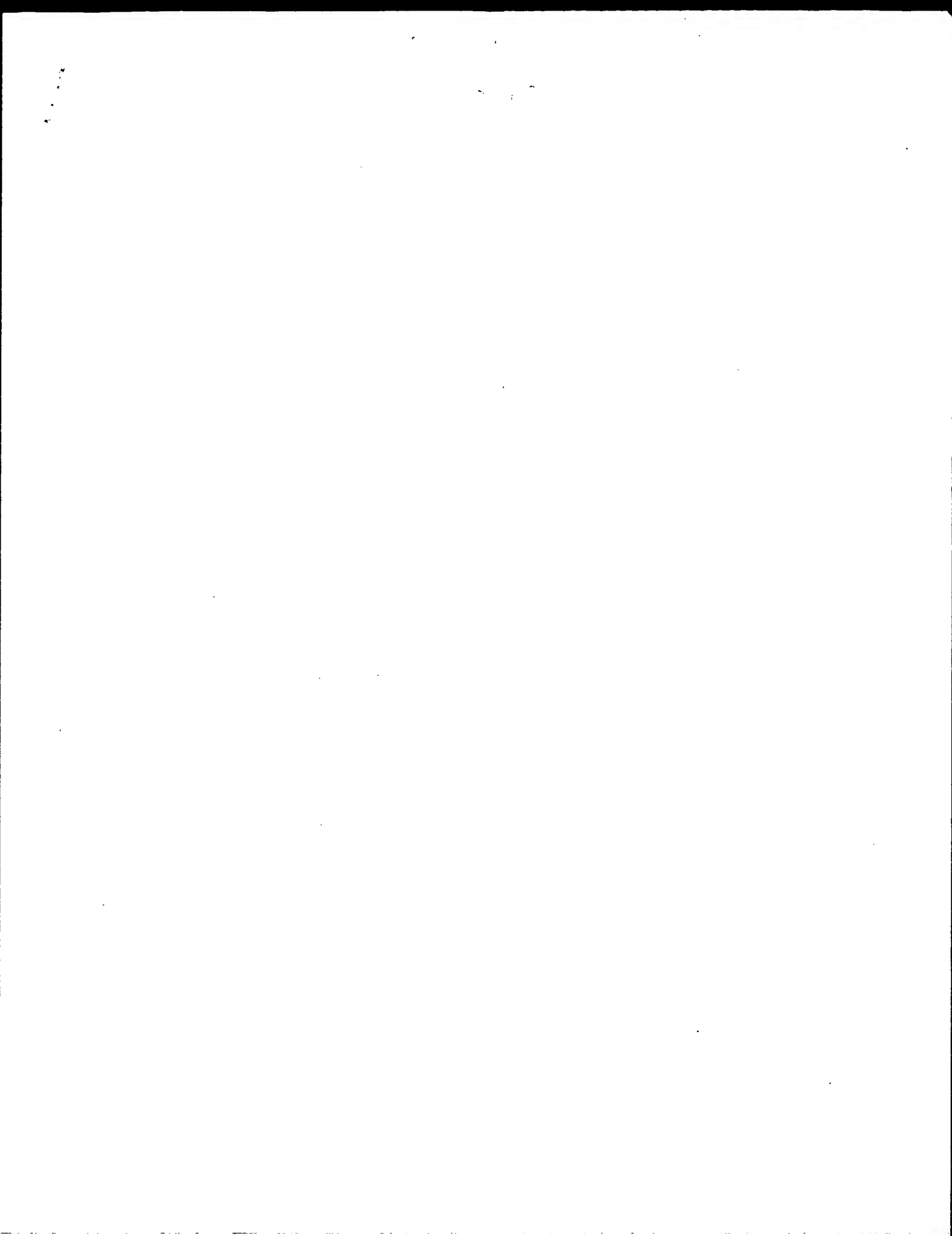
Query Match 43.8%; Score 7; DB 21; Length 429;
 Best Local Similarity 100.0%; Pred. No. 9.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

RESULT 15
 AAM14001
 ID AAM14001 standard; Protein; 433 AA.
 XX
 AC AAM14001;
 XX
 DT 23-MAY-1997 (first entry)
 XX
 DE Enolase protein.
 XX
 KW PCR; polymerase chain reaction; primer; amplify; tyrosine; human; NSE;
 OS enolase; radioisotope; antigen.
 XX
 OS Homo sapiens.
 XX
 PN JF08308584-A.
 XX

PD 26-NOV-1996.
 XX
 PF 19-MAY-1995; 95JP-0145542.
 XX
 PR 19-MAY-1995; 95JP-0145542.
 XX
 PA (EIKE) EIKEN KAGAKU KK.
 XX
 DR WPI; 1997-059703/06.
 XX
 PT Introducing tyrosine residues into a protein for radioisotopic
 PT labelling - by substitution, addition and/or insertion to a DNA
 PT coding for the protein, antigenicity of the protein is unchanged by
 PT labelling
 XX
 PS Disclosure; Page 10-11; 13pp; Japanese.
 XX
 CC This sequence represents the wild type human enolase (NSE) protein. The
 CC primers represented by AAT60282-T60285 were used to amplify tyrosine
 CC introduced versions of this sequence. The introduced tyrosine residues
 CC combine a radioisotope in such a way as to have no substantial effect on
 CC the antigenicity of the protein. The peptides with the introduced
 CC tyrosine residue are prepared by expressing a recombinant DNA sequence,
 CC where the tyrosine residue has been introduced via an insertion or
 CC substitution into the wild type sequence. The peptides can then be used
 CC in radioimmunoassays, as the introduction of the label does not alter
 CC the antigenicity of the protein.
 CC
 XX
 SQ Sequence 433 AA;
 OY 1 LVVGICT 7
 DB 383 LVVGICT 389

Query Match 43.8%; Score 7; DB 18; Length 433;
 Best Local Similarity 100.0%; Pred. No. 9.3;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 8, 2002, 11:47:03
 Job time: 114 sec



C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 72.2%; Score 65; DB 2; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.011;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 362 LVVGLCTGQIKTGAPC 377

RESULT 3
A37210 phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit
N:Alternate names: enolase beta
C:Species: Oryctolagus cuniculus (domestic rabbit)
C:Date: 30-Dec-1991 #sequence_revision 30-Dec-1991 #text_change 05-Aug-1994
C:Accession: A37210
R:Chin, C.C.Q.
J. Protein Chem. 9, 427-432, 1990
A:Title: The primary structure of rabbit muscle enolase.
A:Reference number: A37210; MUID:9113295
A:Accession: A37210
A:Status: preliminary
A:Molecule type: protein
A:Residues: 1-433 <CHI>
C:Superfamily: enolase
C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase
F:1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 4
NOMSB
phosphopyruvate hydratase (EC 4.2.1.11) gamma - human
N:Alternate names: enolase gamma; neuron-specific enolase
C:Species: Homo sapiens (man)
C:Date: 31-Mar-1990 #sequence_revision 31-Mar-1990 #text_change 18-Jun-1999
C:Accession: J00060; S16163; S02077; I56569; S02616; S38303
R:Oliva, D.; Barba, G.; Bardieri, G.; Gallongo, A.; Feo, S.
Gene 79, 355-360, 1989
A:Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.
A:Reference number: J00060; MUID:90006764
A:Accession: J00060
A:Molecule type: mRNA
A:Residues: 1-434 <OLI>
A:Cross-references: GB:M22349; NID:9951199; PIDN:AAB59554.1; PID:g182116; GB:M27833
R:Oliva, D.; Call, L.; Feo, S.; Gallongo, A.
Genomics 10, 157-165, 1991
A:Title: Complete structure of the human gene encoding neuron-specific enolase.
A:Reference number: S16163; MUID:91257823
A:Accession: S16163
A:Molecule type: DNA
A:Residues: 1-434 <OLI>
A:Cross-references: GB:X51956; NID:g31164; PIDN:CAA36215.1; PID:g31165
R:McAleese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.
Eur. J. Biochem. 178, 413-417, 1988
A:Title: Complete amino acid sequence of the neurone-specific gamma isozyme of enolase
A:Reference number: S02077; MUID:89091176
A:Accession: S02077
A:Molecule type: mRNA
A:Residues: 2-3, 'Q', '5-239, 'M', '241-434 <MCA>
A:Cross-references: EMBL:X13120; NID:g31145; PIDN:CAA31512.1; PID:g930063

A:Note: part of this sequence was confirmed by protein sequencing
A:Note: 264-Ala and 395-Ala were also found
R:Van Obberghen, E.; Kamholz, J.; Bishop, J.G.
J. Neurosci. Res. 19, 450-456, 1988

A:Title: Human gamma enolase: isolation of a cDNA clone and expression in normal rat
A:Reference number: I56569; MUID:88259288
A:Accession: I56569

A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA

A:Residues: 'GC', '29-126, 'N', '128-434 <VAN>

A:Cross-references: GB:M36768; NID:g182117; PIDN:AAA5388.1; PID:g182118
R:Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.
FEBS Lett. 222, 139-143, 1987

A:Title: Sequence conservation in the 3'-untranslated regions of neurone-specific
A:Reference number: S02616; MUID:88005129
A:Accession: S02616

A:Status: not compared with conceptual translation
A:Molecule type: mRNA

A:Residues: 425-434 <DAY>

A:Cross-references: GB:Y00691; GB:M27610
R:Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Wilschik, C.M.
Biochim. Biophys. Acta 1158, 120-128, 1993

A:Title: Characterisation of an epitope specific to the neuron-specific isoform of
of Delta/A4-protein.
A:Reference number: S38303; MUID:94002176
A:Accession: S38303

A:Molecule type: protein
A:Residues: 156-173 <HAR>

C:Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in
C:Comment: Thr-191 may be important for the enhanced tolerance to chloride ions of
C:Genetics:

A:Gene: GDB: ENO2
A:Cross-references: GDB:119872; OMIM:131360
A:Map position: 12p13-12p13

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2
C:Complex: homodimer

C:Function:
A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to
A:Pathway: gluconeogenesis; glycolysis

C:Superfamily: enolase
C:Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis

F:2-434/Product: phosphopyruvate hydratase gamma #status predicted <MAT>
F:2/Modified site: blocked amino end (Ser) (in mature form) (probably acetylated) #
F:210/343/Active site: magnesium 2 (Ser) #status predicted

F:245,293,318/Binding site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 72.2%; Score 65; DB 1; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 5

NOMSB
phosphopyruvate hydratase (EC 4.2.1.11) beta - mouse

N:Alternate names: enolase beta
C:Species: Mus musculus (house mouse)

C:Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C:Accession: S17109; S18036; S29675; A33921

R:Ramande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
submitted to the EMBL Data Library, September 1991

A:Reference number: S17109
A:Accession: S17109

A:Molecule type: DNA
A:Residues: 1-434 <LAM>

A:Cross-references: EMBL:X61600; NID:g50848; PIDN:CAA43797.1; PID:g50849
R:Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.

submitted to the EMBL Data Library, October 1991

Query Match 72.2% Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 9

S10247

phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse

N:Alternate names: 2-phosphoglycerate dehydratase; enolase gamma

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence_revision 12-Feb-1993 #text_change 22-Jun-1999

C:Accession: S10247

R:Kaghad, M.; Dumont, X.; Chalou, P.; Lellias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res 18, 3638, 1990

A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.

A:Reference number: S10246; MUID:90301487

A:Accession: S10247

A:Molecule type: mRNA

A:Residues: 1-434 <KRG>

A:Cross-references: EMBL:X52380; NID:g55494; PIDN:CAA3606.1; PID:g55495

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match

Best Local Similarity 72.2% Score 65; DB 2; Length 434;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 10

A29170

phosphopyruvate hydratase (EC 4.2.1.11) alpha - human

N:Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha

C:Species: Homo sapiens (man)

C:Date: 19-Nov-1988 #sequence_revision 19-Nov-1988 #text_change 20-Jun-2000

C:Accession: S11696; A29170; S52858; A39183

R:Giallongo, A.; Oliva, D.; Calli, L.; Barba, G.; Barbieri, G.; Feo, S.

Eur. J. Biochem. 190, 567-573, 1990

A:Title: Structure of the human gene for alpha-enolase.

A:Reference number: S11696; MUID:90323004

A:Accession: S11696

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-434 <GIA>

A:Cross-references: EMBL:X16288; NID:g31172; PIDN:CAA34360.1; PID:g1167843

A:Note: the nucleotide sequence was submitted to the EMBL data library, August 1989

R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Shown, L.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986

A:Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human alpha

A:Reference number: A29170; MUID:86313654

A:Accession: A29170

A:Molecule type: mRNA

A:Residues: 1-434 <G12>

A:Cross-references: GB:M4328; NID:g182113; PIDN:AAA5387.1; PID:g182114

A:Note: the authors translated the codon AAG for residue 193 as His

R:Walter, M.; Laidenberger, F.A.; Schweppe, K.W.; Berg, H.; Northmann, W.

submitted to the EMBL data library, February 1995

A:Description: Autoreactive epitopes within the human alpha-enolase and their recognition

A:Reference number: S52858

A:Accession: S52858

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-251, 'S', 253-434 <NAL>

A:Cross-references: EMBL:X84907; NID:g693932; PIDN:CAA59331.1; PID:g693933

A:Experimental source: endometrium carcinoma cell line HEC-1B

R:Milles, L.A.; Dahlberg, C.M.; Plescia, J.; Fellez, J.; Kato, K.; Plov, E.F.

Biochemistry 30, 1682-1691, 1991

A:Title: Role of cell-surface lysines in plasminogen binding to cells: identification

A:Reference number: A39183; MUID:91129243

A:Accession: A39183

A:Molecule type: protein

A:Residues: 170-182, 'I', 184, 'R', 186-190, 245-252 <MLT>

C:Genetics:

A:Gene: GDB:ENO1

A:Cross-references: GDB:119871; OMIM:172430

A:Map position: 1p36-1p36

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2

C:Function:

A:Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosph

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesiu

F:2-434/Product: phosphopyruvate hydratase alpha #status predicted <MAN>

Query Match 72.2% Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 11

A2132

phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck

N:Alternate names: enolase alpha; tau-crystallin

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 21-May-1990 #sequence_revision 21-May-1990 #text_change 21-Jun-2000

C:Accession: A32132

R:Wistow, G.J.; Lietman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz, J.

J. Cell Biol. 107, 2729-2736, 1988

A:Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens s

A:Reference number: A27250; MUID:89079778

A:Accession: A32132

A:Molecule type: mRNA

A:Residues: 1-434 <WIS>

A:Cross-references: GB:X14195; NID:g62455; PIDN:CAA32409.1; PID:g62456

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 72.2% Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
||||| |||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 12

S02072

phosphopyruvate hydratase (EC 4.2.1.11) beta - rat

N:Alternate names: enolase beta; enolase, muscle-specific

C:Species: Rattus norvegicus (Norway rat)

C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 22-Jun-1999

C:Accession: S02072

R:Ohshima, Y.; Mitsui, H.; Takayama, Y.; Kushiya, E.; Sakimura, K.; Takahashi, Y.

FEBS Lett. 242, 425-430, 1989

A:Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-p

A:Reference number: S02072; MUID:89121113

A:Accession: S02072

A:Molecule type: mRNA

A:Residues: 1-434 <OHS>

A:Cross-references: EMBL:X00979; NID:g57781; PIDN:CAA68788.1; PID:g57782

A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40.

C:Superfamily: enolase
C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 13

S06756

phosphopyruvate hydratase (EC 4.2.1.11) beta - human

N:Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, muscle
C:Species: Homo sapiens (man)
C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 22-Jun-1999

C:Accession: S06756; S14759; S15933; S33330; S08685; S31650

R:Pescharia, M.; Hinks, L.J.; Day, I.N.M.
Nucleic Acids Res. 17, 8862, 1989

A:Title: Structure of human muscle (beta) enolase mRNA and protein deduced from a genomic
A:Reference number: S06756; MUID:90067857

A:Accession: S06756

A:Molecule type: mRNA

A:Residues: 1-434 <PE>

A:Cross-references: EMBL:X16504; NID:g31169; PIDN:CAA34513.1; PID:g31170

R:Pescharia, M.; Day, I.N.M.

Biochem. J. 275, 427-433, 1991

A:Title: Molecular structure of the human muscle-specific enolase gene (ENOS).

A:Reference number: S14759; MUID:91222137

A:Accession: S14759

A>Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-434 <PE>

A:Cross-references: EMBL:X55976

R:Call, L.; Feo, S.; Oliva, D.; Gallongo, A.

Nucleic Acids Res. 18, 1893, 1990

A:Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase (MSE).

A:Reference number: S15933; MUID:90245587

A:Accession: S15933

A:Molecule type: mRNA

A:Residues: 1-84, 'A', 86-161, 'K', 163-434 <CAL>

A:Cross-references: EMBL:X51957; NID:g34788; PIDN:CAA36216.1; PID:g34789

R:Gallongo, A.; Venturilla, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.

Eur. J. Biochem. 214, 367-374, 1993

A:Title: Structural features of the human gene for muscle-specific enolase. Differential

A:Reference number: S33330; MUID:93292497

A:Accession: S33330

A>Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-161, 'K', 163-434 <GIA>

A:Cross-references: EMBL:X56832; NID:g31166; PIDN:CAA40163.1; PID:g31167

A:Note: The nucleotide sequence was submitted to the EMBL Data Library, November 1990

C:Genetics:

A:Gene: GDB:ENOS

A:Cross-references: GDB:119873; OMIM:131370

A:Map position: 17pter-17p12

A:Insertions: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle; skele

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 14

JC4186

phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken

N:Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000

C:Accession: JC4186

R:Tanaka, M.; Maeda, K.; Nakashima, K.

J. Biochem. 117, 554-559, 1995

A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-p

A:Reference number: JC4186; MUID:9535305

A:Accession: JC4186

A:Molecule type: mRNA

A:Residues: 1-434 <TRAN>

A:Cross-references: DDBJ:D37900; NID:g974175; PIDN:BA07132.1; PID:g974176

A:Experimental source: Brain

C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported

rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all t

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein

F/44/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

RESULT 15

JC4187

phosphopyruvate hydratase (EC 4.2.1.11) beta chain - chicken

N:Alternate names: beta-2-phospho-D-glycerate hydrolase; enolase

C:Species: Gallus gallus (chicken)

C:Date: 14-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000

C:Accession: JC4187

R:Tanaka, M.; Maeda, K.; Nakashima, K.

J. Biochem. 117, 554-559, 1995

A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-p

A:Reference number: JC4186; MUID:9535305

A:Accession: JC4187

A:Molecule type: mRNA

A:Residues: 1-434 <TRAN>

A:Cross-references: DDBJ:D37901; NID:g974177; PIDN:BA07133.1; PID:g1616990

C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported

rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all t

C:Superfamily: enolase

C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase; phosphoprotein

F/1/Modified site: acetylated amino end (Met) #status experimental

Query Match 72.2%; Score 65; DB 2; Length 434;
Best Local Similarity 81.2%; Pred. No. 0.012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
|||||
DB 384 LVVGLCTGQIKTGAPC 399

Search completed: May 8, 2002, 11:45:46
Job time: 102 sec

CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 XX
 SQ Sequence 16 AA;

Query Match 100.0%; Score 90; DB 20; Length 16;
 Best Local Similarity 100.0%; Pred. No. 4.8e-06;
 Matches 15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGPAC 16
 DB 1 LVVGLCTGQIKTGPAC 16

RESULT 2

AAV43204
 ID AAV43204 standard; peptide: 16 AA.

XX
 AC AAV43204;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #14.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.

XX 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 4; Page 21; 37pp; English.

QY This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 XX

SQ Sequence 16 AA;

Query Match 86.7%; Score 78; DB 20; Length 16;

Best Local Similarity 93.8%; Pred. No. 0.00021;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGPAC 16
 |||||

DB 1 LVVGLCTGQIKTGPAC 16

RESULT 3

AAV43197
 ID AAV43197 standard; peptide: 17 AA.

XX
 AC AAV43197;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #7.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.

XX 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 3; Page 21; 37pp; English.

QY This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 XX

SQ Sequence 17 AA;

Query Match 86.7%; Score 78; DB 20; Length 17;

Best Local Similarity 93.8%; Pred. No. 0.00021;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGPAC 16
 DB 1 LVVGLCTGQIKTGPAC 16

RESULT 4

AAV43198
 ID AAV43198 standard; peptide: 17 AA.

XX
 AC AAV43198;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #8.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 XX platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.
 XX 14-OCT-1999.
 PD 30-MAR-1999; 99WO-IL00190.
 XX 02-APR-1998; 98IL-0123925.
 PR (YEDA) YEDA RES & DEV CO LTD.
 XX Shinitzky M, Deckmann M;
 XX WPI: 1999-611037/52.
 DR
 XX
 PT New peptides useful for diagnosis of schizophrenia -
 PS Claim 3; Page 21; 37pp; English.
 XX
 CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 SQ Sequence 17 AA;

Query Match 86.7%; Score 78; DB 20; Length 17;
 Best Local Similarity 93.8%; Pred. No. 0.00021;
 Matches 15; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16
 |||||
 Db 1 LVVGLCTPQIKTGPAC 16

RESULT 5
 AAY43202
 ID AAY43202 standard; peptide; 16 AA.
 XX
 AC AAY43202;
 XX
 DT 11-JAN-2000 (first entry)
 DE
 XX Schizophrenic derived antibody binding epitope #12.
 XX
 KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.
 XX
 OS Synthetic.
 XX
 PN WO9951725-A2.
 XX 14-OCT-1999.
 PD 30-MAR-1999; 99WO-IL00190.
 XX 02-APR-1998; 98IL-0123925.
 PR (YEDA) YEDA RES & DEV CO LTD.
 PA Shinitzky M, Deckmann M;
 PI WPI: 1999-611037/52.
 DR
 XX
 PT New peptides useful for diagnosis of schizophrenia -
 PS Claim 4; Page 21; 37pp; English.
 XX

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 SQ Sequence 16 AA;

Query Match 72.2%; Score 65; DB 20; Length 16;
 Best Local Similarity 81.2%; Pred. No. 0.012;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16
 |||||
 Db 1 LVVGLCTPQIKTGPAC 16

RESULT 6
 AAY43196
 ID AAY43196 standard; peptide; 17 AA.
 XX
 AC AAY43196;
 XX
 DT 11-JAN-2000 (first entry)
 DE
 XX Schizophrenic derived antibody binding epitope #6.
 XX
 KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KW platelet-associated antibody; diagnosis.
 XX
 OS Synthetic.
 XX
 PN WO9951725-A2.
 XX 14-OCT-1999.
 PD 30-MAR-1999; 99WO-IL00190.
 XX 02-APR-1998; 98IL-0123925.
 PR (YEDA) YEDA RES & DEV CO LTD.
 PA Shinitzky M, Deckmann M;
 PI WPI: 1999-611037/52.
 DR
 XX
 PT New peptides useful for diagnosis of schizophrenia -
 PS Claim 3; Page 21; 37pp; English.
 XX

CC This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 SQ Sequence 17 AA;

Query Match 72.2%; Score 65; DB 20; Length 17;
 Best Local Similarity 81.2%; Pred. No. 0.013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGPAC 16

Db 1 lvvglcgqiktgapc 16

RESULT 7

AAV43195 standard; peptide: 18 AA.

AAV43195;

11-JAN-2000 (first entry)

Schizophrenic derived antibody binding epitope #5.

Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

Synthetic.

WO9951725-A2.

14-OCT-1999.

30-MAR-1999; 99WO-IL00190.

02-APR-1998; 98IL-0123925.

(YEDA) YEDA RES & DEV CO LTD.

Shinitzky M, Deckmann M;

WPI; 1999-611037/52.

New peptides useful for diagnosis of schizophrenia -

Claim 3; Page 21; 37pp; English.

This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.

Sequence 18 AA;

Query Match 72.2%; Score 65; DB 20; Length 18;

Best Local Similarity 81.2%; Pred. No. 0.013;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCOIKTGAPAC 16

Db 2 lvvglcgqiktgapc 17

RESULT 8

AAV43194 standard; peptide: 19 AA.

AAV43194;

11-JAN-2000 (first entry)

Schizophrenic derived antibody binding epitope #4.

Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

Synthetic.

XX WO9951725-A2.

XX 14-OCT-1999.

XX 30-MAR-1999; 99WO-IL00190.

XX 02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

XX Claim 3; Page 21; 37pp; English.

This sequence is a peptide of the invention, which binds antibodies found in elevated levels in body fluids of schizophrenic patients. The peptide is useful in an assay for the diagnosis of schizophrenia, by binding the peptide to a platelet-containing fraction of blood, or a fraction containing platelet-associated antibodies (PAA) shed from the platelets, or preferably whole blood. The new peptides are able to differentiate between plasma samples from schizophrenic and non-schizophrenic patients, and can do so without having to first isolate the platelet-associated antibodies (PAA) fraction.

Sequence 19 AA;

Query Match 72.2%; Score 65; DB 20; Length 19;

Best Local Similarity 81.2%; Pred. No. 0.014;

Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCOIKTGAPAC 16

Db 3 lvvglcgqiktgapc 18

RESULT 9

AAV43193 standard; peptide: 20 AA.

AAV43193;

11-JAN-2000 (first entry)

Schizophrenic derived antibody binding epitope #3.

Schizophrenic derived antibody; binding epitope; schizophrenia;
platelet-associated antibody; diagnosis.

Synthetic.

WO9951725-A2.

14-OCT-1999.

30-MAR-1999; 99WO-IL00190.

02-APR-1998; 98IL-0123925.

XX (YEDA) YEDA RES & DEV CO LTD.

XX Shinitzky M, Deckmann M;

XX WPI; 1999-611037/52.

XX New peptides useful for diagnosis of schizophrenia -

XX Claim 3; Page 21; 37pp; English.

XX This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 XX Sequence 20 AA;
 SQ

Query Match 72.2%; Score 65; DB 20; Length 20;
 Best Local Similarity 81.2%; Pred. No. 0.014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCOIKTGPAC 16
 ||||| |||||
 Db 4 lvvgltcgtgiktgapc 19

RESULT 10
 AAY43192
 ID AAY43192 standard; peptide; 28 AA.
 XX
 AC AAY43192;
 DT 11-JAN-2000 (first entry)
 XX
 DE Schizophrenic derived antibody binding epitope #2.
 XX
 KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 KM platelet-associated antibody; diagnosis.
 XX
 OS Synthetic.
 XX
 PN WO9951725-A2.
 XX
 PD 14-OCT-1999.
 XX
 PF 30-MAR-1999; 99WO-IL00190.
 XX
 PR 02-APR-1999; 98IL-0123925.
 XX
 PA (YEDA) YEDA RES & DEV CO LTD.
 XX
 PI Shinitzky M, Deckmann M;
 XX
 DR WPI: 1999-611037/52.
 XX
 PT New peptides useful for diagnosis of schizophrenia -
 PT
 PS Claim 3; Page 21; 37pp; English.
 XX

This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 XX Sequence 28 AA;
 SQ

Query Match 72.2%; Score 65; DB 20; Length 28;
 Best Local Similarity 81.2%; Pred. No. 0.019;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCOIKTGPAC 16
 ||||| |||||
 Db 12 lvvgltcgtgiktgapc 27

RESULT 11
 AAB42064
 ID AAB42064 standard; Protein; 429 AA.
 XX
 AC AAB42064;
 DT 08-FEB-2001 (first entry)
 XX
 DE Human ORFX ORF1828 polypeptide sequence SEQ ID NO:3656.
 XX
 KW Human; open reading frame; ORFX; detection; cytosolic; hepatotropic;
 KW vulnery; antipsoatic; antiparkinsonian; neurotropic; neuroprotective;
 KW anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant;
 KW immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic;
 KW hypotensive; dermatological; immunosuppressive; antiinflammatory;
 KW antiviral; antibacterial; antifungal; antirheumatic; antihypertensive;
 KW antinaemic; gene therapy; cancer; proliferative disorder; hypertension;
 KW neurodegenerative disorder; osteoarthritis; graft vs host disease;
 KW cardiovascular disease; diabetes mellitus; hypothyroidism; SCID; AIDS;
 KW cholesterol ester storage; systemic lupus erythematosus; infection;
 KW severe combined immunodeficiency; malaria; autoimmune disorder; asthma;
 KW allergy; aplastic anaemia; nocturnal haemoglobinuria; burn; wound;
 KW bone damage; cartilage damage; antiinflammatory disease; coagulation;
 KW thrombosis; contraceptive.
 KW
 XX Homo sapiens.
 OS
 XX
 PN WO200058473-A2.
 PD 05-OCT-2000.
 XX
 PF 31-MAR-2000; 2000WO-US08621.
 XX
 PR 31-MAR-1999; 99US-0127607.
 PR 02-APR-1999; 99US-0127636.
 PR 05-APR-1999; 99US-0127728.
 PR 30-MAR-2000; 2000US-0540763.
 XX
 PA (CURA-) CURAGEN CORP.
 XX
 PI Shimkets RA, Leach M;
 PT
 DR N-PSDB; AAC76273.
 XX
 PT Novel nucleic acids and peptides derived from open reading frame X,
 PT useful for treating e.g. cancers, proliferative disorders,
 PT neurodegenerative disorders and cardiovascular disease -
 XX
 PS Claim 11; Page 2810-2811; 5507pp; English.
 XX

AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397,
 CC which represent the human ORFX open reading frames 1 to 3161. The ORFX
 CC sequences have activities such as: cytosolic; hepatotropic; vulnery;
 CC antipsoatic; antiparkinsonian; neurotropic; neuroprotective;
 CC osteopathic; anticonvulsant; antiarthritic; immunosuppressant;
 CC immunostimulant; cardiant; thrombolytic; coagulant; vasotropic;
 CC antidiabetic; hypotensive; dermatological; immunosuppressive;
 CC antiinflammatory; antibacterial; antiviral; antifungal; antirheumatic;
 CC antihypertensive; antinaemic. The sequences can be used for determining
 CC the presence of or predisposition to, or preventing or treating
 CC pathological conditions associated with an ORFX-associated disorder. The
 CC nucleic acids can be used to express ORFX proteins in gene therapy
 CC vectors. The proteins and nucleic acids may be used to treat cancers,
 CC proliferative disorders, neurodegenerative disorders, osteoarthritis,
 CC graft vs host disease, cardiovascular disease, diabetes mellitus,
 CC hypertension, hypothyroidism, cholesterol ester storage, systemic lupus
 CC erythematosus, severe combined immunodeficiency (SCID), AIDS, viral,

CC bacterial or fungal infection, malaria, autoimmune disorders, asthma,
CC allergies, aplastic anaemia, burns, wounds, bone and cartilage damage,
CC nocturnal haemoglobinuria, antiinflammatory disease; to enhance
CC coagulation; to inhibit thrombosis; and as a contraceptive.
XX

SO Sequence 429 AA;

Query Match 72.2%; Score 65; DB 21; Length 429;
Best Local Similarity 81.2%; Pred. No. 0.2;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCQIKTGAPC 16
| | | | | | | | | | | | | | | | |
Db 379 lvvgltctgqiktgapc 394

RESULT 12
AAW14001
ID AAW14001 standard; Protein; 433 AA.
XX
AC AAW14001;
XX

DT 23-MAY-1997 (first entry)
XX

DE Enolase protein.

KW PCR; polymerase chain reaction; primer; amplify; tyrosine; human; NSE;
KM enolase; radioisotope; antigen.

XX Homo sapiens.

XX JP08308584-A.

PD 26-NOV-1996.

PF 19-MAY-1995; 95JP-0145542.

PR 19-MAY-1995; 95JP-0145542.

PA (EIKE) EIKEN KAGAKU KK.

DR WPI; 1997-059703/06.

PT Introducing tyrosine residues into a protein for radioisotopic
PT labelling - by substitution, addition and/or insertion to a DNA
PT coding for the protein, antigenicity of the protein is unchanged by
PT labelling

PS Disclosure: Page 10-11; 13pp: Japanese.

XX This sequence represents the wild type human enolase (NSE) protein. The
CC primers represented by AAT60282-T60285 were used to amplify tyrosine
CC introduced versions of this sequence. The introduced tyrosine residues
CC combine a radioisotope in such a way as to have no substantial effect on
CC the antigenicity of the protein. The peptides with the introduced
CC tyrosine residue are prepared by expressing a recombinant DNA sequence,
CC where the tyrosine residue has been introduced via an insertion or
CC substitution into the wild type sequence. The peptides can then be used
CC in radioimmunoassays, as the introduction of the label does not alter
CC the antigenicity of the protein.

SO Sequence 433 AA;

Query Match 72.2%; Score 65; DB 18; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.2;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCQIKTGAPC 16
| | | | | | | | | | | | | | | | |
Db 383 lvvgltctgqiktgapc 398

RESULT 13
AAW54357
ID AAW54357 standard; protein; 433 AA.
XX
AC AAW54357;
XX

DT 14-AUG-1998 (first entry)
XX

DE Alpha Enolase.

KW Endometrium; hyperplasia; adenocarcinoma; proliferative phase;
KM 2D gel electrophoresis; detection.

XX Homo sapiens.

PN WO9810291-A1.

PD 12-MAR-1998.

PF 05-SEP-1997; 97WO-GB02394.

PR 08-APR-1997; 97GB-0007132.

PR 06-SEP-1996; 96GB-0018600.

PA (CLIN) CENT CLINICAL & BASIC RES.

PI Byrjalsen I, Fey SJ, Larsen P;

DR WPI; 1998-207057/18.

XX Biochemical markers of human endometrium - useful for, e.g.
PT diagnosis of hyperplasia and adenocarcinoma

PS Disclosure: Page 21; 77pp; English.

CC Proteins AAW54349-W54364 are examples of proteins produced in the
CC endometrium during the hyperplasia, adenocarcinoma or proliferative
CC phase of the endometrium. The presence and quantities of these proteins
CC can be detected using 2D gel electrophoresis comparison of cell lysates.
CC The proteins can be used as biochemical markers to detect the phase of
CC the endometrium and can be measured in body fluids, obviating the need
CC for endometrial biopsies.

SO Sequence 433 AA;

Query Match 72.2%; Score 65; DB 19; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.2;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTCQIKTGAPC 16
| | | | | | | | | | | | | | | | |
Db 383 lvvgltctgqiktgapc 398

RESULT 14
AAV43200
ID AAV43200 standard; peptide; 16 AA.

AC AAV43200;

DT 11-JAN-2000 (first entry)

XX Schizophrenic derived antibody binding epitope #10.

DE Schizophrenic derived antibody; binding epitope; schizophrenia;
KW platelet-associated antibody; diagnosis.

XX Synthetic.

OS WO9951725-A2.

XX

PD 14-OCT-1999.
 XX 30-MAR-1999; 99WO-IL00190.
 XX 02-APR-1998; 98IL-0123925.
 XX (YEDA) YEDA RES & DEV CO LTD.
 XX Shinitzky M, Deckmann M;
 DR WPI; 1999-611037/52.
 XX New peptides useful for diagnosis of schizophrenia -
 PT Claim 4; Page 21; 37pp; English.
 PS This sequence is a peptide of the invention, which binds antibodies found
 CC in elevated levels in body fluids of schizophrenic patients. The peptide
 CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 SQ Sequence 16 AA;

Query Match 67.8%; Score 61; DB 20; Length 16;
 Best Local Similarity 80.0%; Pred. No. 0.042;
 Matches 12; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 2 VVGLCTCQIKTGAPC 16
 |||||
 DB 1 VVGLCTGQIKTGAPC 15

RESULT 15

AAV43203
 ID AAV43203 standard; peptide; 15 AA.

AC AAV43203;

DT 11-JAN-2000 (first entry)

DE Schizophrenic derived antibody binding epitope #13.

KW Schizophrenic derived antibody; binding epitope; schizophrenia;
 platelet-associated antibody; diagnosis.

OS Synthetic.

PN WO9951725-A2.

PD 14-OCT-1999.

PF 30-MAR-1999; 99WO-IL00190.

PR 02-APR-1998; 98IL-0123925.

PA (YEDA) YEDA RES & DEV CO LTD.

PI Shinitzky M, Deckmann M;

DR WPI; 1999-611037/52.

PT New peptides useful for diagnosis of schizophrenia -

PS Claim 4; Page 21; 37pp; English.

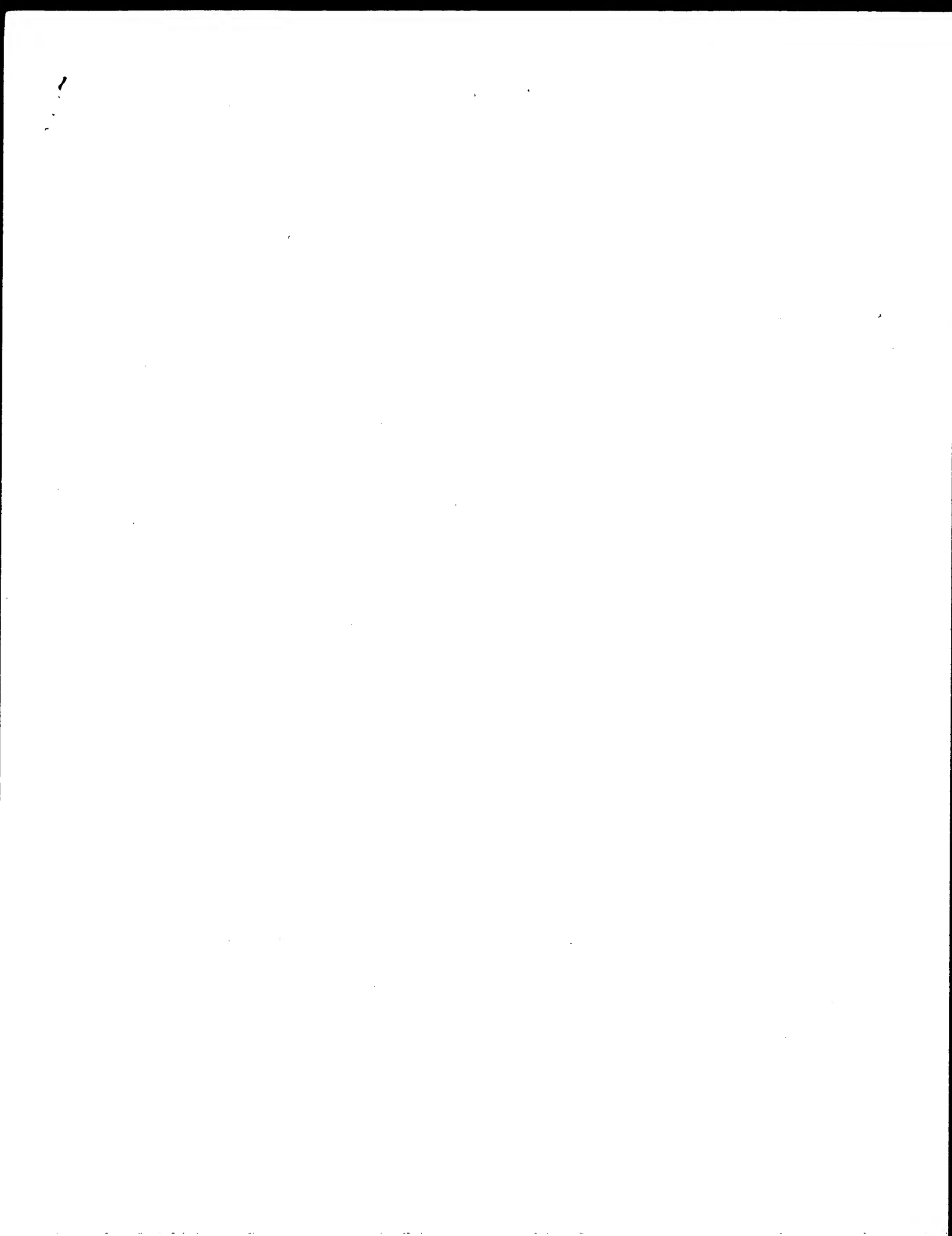
CC This sequence is a peptide of the invention, which binds antibodies found
 in elevated levels in body fluids of schizophrenic patients. The peptide

CC is useful in an assay for the diagnosis of schizophrenia, by binding the
 CC peptide to a platelet-containing fraction of blood, or a fraction
 CC containing platelet-associated antibodies (PAA) shed from the platelets,
 CC or preferably whole blood. The new peptides are able to differentiate
 CC between plasma samples from schizophrenic and non-schizophrenic patients,
 CC and can do so without having to first isolate the platelet-associated
 CC antibodies (PAA) fraction.
 CC
 SQ Sequence 15 AA;

Query Match 64.4%; Score 58; DB 20; Length 15;
 Best Local Similarity 92.3%; Pred. No. 0.1;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTG 13
 |||||
 DB 1 LVVGLCTGQIKTG 13

Search completed: May 8, 2002, 11:45:08
 Job time: 209 sec



Query Match 43.8%; Score 7; DB 4; Length 154;
Best Local Similarity 100.0%; Pred. No. 3.9;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 104 LVVGLCT 110

RESULT 2

O9NG70

PRELIMINARY; PRT; 159 AA.

AC O9NG70; PRELIMINARY; PRT; 159 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Peripatus sp. 'Per3'.
OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.
OX NCBI_TaxID=126380;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PER3248.407;
RA Regier J.C., Shultz J.W.;
RT Enolase as a phylogenetic marker."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1 COPROCTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1 SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF258667; AAF72638.1; -
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; ENOLASE; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17582 MW; 840E266ACD36D3CD CRC64;

Query Match 43.8%; Score 7; DB 5; Length 159;
Best Local Similarity 100.0%; Pred. No. 4;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 138 LVVGLCT 144

RESULT 3

O9NG71

PRELIMINARY; PRT; 251 AA.

AC O9NG71; PRELIMINARY; PRT; 251 AA.
DT 01-OCT-2000 (TREMBlrel. 15, Created)
DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Limulus polyphemus (Atlantic horseshoe crab).
OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
OX NCBI_TaxID=6850;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=LPO156_406;

RA Regier J.C., Shultz J.W.;
RT "Enolase as a phylogenetic marker."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
CC -1 COPROCTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1 SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF258666; AAF72637.2; -
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; ENOLASE; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Glycolysis; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 251
SQ SEQUENCE 251 AA; 27452 MW; DEB7B1BA7A87693F CRC64;

Query Match 43.8%; Score 7; DB 5; Length 251;
Best Local Similarity 100.0%; Pred. No. 5.7;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 230 LVVGLCT 236

RESULT 4

O9BT62

PRELIMINARY; PRT; 272 AA.

AC O9BT62; PRELIMINARY; PRT; 272 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE UNKNOWN (PROTEIN FOR IMAGE:3629132) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
CC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CHORIOCARCINOMA;
RA Strausberg R.;
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004325; AAH04325.1; -
FT NON_TER 1
FT NON_TER 272
SQ SEQUENCE 272 AA; 29883 MW; 08F1755ADEA88BDC CRC64;

Query Match 43.8%; Score 7; DB 4; Length 272;
Best Local Similarity 100.0%; Pred. No. 6.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 222 LVVGLCT 228

RESULT 5

O99KT7

PRELIMINARY; PRT; 353 AA.

AC O99KT7; PRELIMINARY; PRT; 353 AA.
DT 01-JUN-2001 (TREMBlrel. 17, Created)
DT 01-JUN-2001 (TREMBlrel. 17, Last sequence update)
DE SIMILAR TO ENOLASE 1, ALPHA NON-NEURON (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Strausberg R.;
 RL Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC004017; AA04017.1; -
 FT NON_TER 1
 SQ SEQUENCE 353 AA; 38299 MW; 2DBD375CE1C26A43 CRC64;

Query Match 43.8%; Score 7; DB 11; Length 353;
 Best Local Similarity 100.0%; Pred. No. 7.5;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
 Db 303 LVGLCT 309

RESULT 6
 Q9W6D3 PRELIMINARY; PRT; 373 AA.
 AC Q9W6D3;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Pelusios subdiger.
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Testudines; Pleurodira; Pelomedusidae; Pelusios.
 OX NCBI_Taxid=88690;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99141276; PubMed=9974396;
 RA Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."
 RL Science 283:998-1001(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL; AF115859; AAD20346.1; -
 DR HSSP; P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; Enolase; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT ACT_SITE 373
 FT METAL 322
 FT METAL 334
 SQ SEQUENCE 373 AA; 40259 MW; 39B5C8BB467BD04 CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
 Db 365 LVGLCT 371

RESULT 7
 Q9W6D2

ID Q9W6D2 PRELIMINARY; PRT; 373 AA.
 AC Q9W6D2;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Trachemys scripta (Red-eared slider turtle) (Pseudemys scripta).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidea; Emydidae; Trachemys.
 OX NCBI_Taxid=34903;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99141276; PubMed=9974396;
 RA Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."
 RL Science 283:998-1001(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL; AF115858; AAD20345.1; -
 DR HSSP; P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; Enolase; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT ACT_SITE 373
 FT METAL 322
 FT METAL 334
 SQ SEQUENCE 373 AA; 40272 MW; 05BBFAFAD64BF99 CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVGLCT 7
 Db 365 LVGLCT 371

RESULT 8
 Q9W6D1 PRELIMINARY; PRT; 373 AA.
 AC Q9W6D1;
 DT 01-NOV-1999 (Tremblrel. 12, Created)
 DT 01-NOV-1999 (Tremblrel. 12, Last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Eumeces inexpectatus (southeastern five-lined skink).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Scleroglossa; Scincomorpha; Scincoidae;
 OC Scincidae; Eumeces.
 OX NCBI_Taxid=38930;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99141276; PubMed=9974396;
 RA Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."
 RL Science 283:998-1001(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).

CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF115857; AAD20344.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KM Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT ACT_SITE 373 373 BY SIMILARITY.
 FT METAL 334 334 MAGNESIUM (BY SIMILARITY).
 FT METAL 334 334
 SQ SEQUENCE 373 AA; 40398 MW; 5D46A0D51F63982A CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
 Db 365 LVVGLCT 371

RESULT 9
 O9W6D0 PRELIMINARY; PRT; 373 AA.
 AC O9W6D0;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ALPHA ENOLASE (FRAGMENT).
 OS Sphenodon punctatus (Hatteria) (Tuatara).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Rhynchocephalia; Sphenodontidae; Sphenodon.
 NC NCB1_TaxID=8508;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99141276; PubMed=9974396;
 RA Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."; Science 283:998-1001(1999).
 RL EMBL: AF115856; AAD20343.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 FT NON_TER 1
 FT ACT_SITE 373 373
 FT METAL 334 334
 SQ SEQUENCE 373 AA; 40440 MW; 1B8D2143C83F865D CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
 Db 365 LVVGLCT 371

RESULT 10
 O9W6C9 PRELIMINARY; PRT; 373 AA.
 AC O9W6C9;
 DT 01-NOV-1999 (TREMBlrel. 12, Created)
 DT 01-NOV-1999 (TREMBlrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)

DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Caiman crocodilus (Spectacled caiman) (Caiman sclerops).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Archosauria; Crocodylidae; Alligatorinae; Caiman.
 NC NCB1_TaxID=8499;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=99141276; PubMed=9974396;
 RA Hedges S.B., Poling L.L.;
 RT "A molecular phylogeny of reptiles."; Science 283:998-1001(1999).
 RL Science 283:998-1001(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF115855; AAD20342.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KM Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT ACT_SITE 373 373 BY SIMILARITY.
 FT METAL 334 334 MAGNESIUM (BY SIMILARITY).
 FT METAL 334 334
 SQ SEQUENCE 373 AA; 40396 MW; 9F9020B86F6657A CRC64;

Query Match 43.8%; Score 7; DB 13; Length 373;
 Best Local Similarity 100.0%; Pred. No. 7.8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
 Db 365 LVVGLCT 371

RESULT 11
 O9NG67 PRELIMINARY; PRT; 383 AA.
 AC O9NG67;
 DT 01-OCT-2000 (TREMBlrel. 15, Created)
 DT 01-OCT-2000 (TREMBlrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBlrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Tomocerus sp. 'Tom'.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Collembola;
 OC Arthropoda; Insecta; Entomobryoidae; Tomoceridae; Tomocerus.
 NC NCB1_TaxID=111305;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=TOM23_406;
 RA Regier J.C., Shultz J.W.;
 RT "Enolase as a phylogenetic marker."; Submitted (Apr-2000) to the EMBL/Genbank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF258670; AAF72641.1; -.
 DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW GLYCOLYSIS; Lyase; Magnesium.
 FT NON_TER 1
 FT 383
 SO SEQUENCE 383 AA; 41326 MW; 4523F005F6A5E579 CRC64;

Query Match 43.8%; Score 7; DB 5; Length 383;
 Best Local Similarity 100.0%; Pred. No. 8;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 363 LVVGLCT 369

RESULT 12
 O9PTX6 PRELIMINARY; PRT; 394 AA.
 AC O9PTX6;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 GN ENOLASE-1.
 OS Lampetra reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 CC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_TaxID=7753;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes";
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL; AB025329; BAA88482.1; -.
 DR HSSP; P56252; 1PD2.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW GLYCOLYSIS; Lyase; Magnesium.
 FT NON_TER 1
 FT 394 AA; 42583 MW; BC585F6EC712A3D2 CRC64;
 SO SEQUENCE

Query Match 43.8%; Score 7; DB 13; Length 394;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 345 LVVGLCT 351

RESULT 13
 O9PTX5 PRELIMINARY; PRT; 395 AA.
 AC O9PTX5;

DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 GN ENOLASE-2.
 OS Lampetra reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 CC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_TaxID=7753;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes";
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL; AB025330; BAA88483.1; -.
 DR HSSP; P56252; 1PD2.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW GLYCOLYSIS; Lyase; Magnesium.
 FT NON_TER 1
 FT 395 AA; 43266 MW; 8591D68662DA8544 CRC64;
 SO SEQUENCE

Query Match 43.8%; Score 7; DB 13; Length 395;
 Best Local Similarity 100.0%; Pred. No. 8.1;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
 |||||
 Db 345 LVVGLCT 351

RESULT 14
 O905F7 PRELIMINARY; PRT; 395 AA.
 AC O905F7;
 DT 01-MAY-2000 (TREMBLrel. 13, Created)
 DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 GN Eptatretus burgeri (Inshore hagfish).
 OS Eptatretus; Metazoa; Chordata; Craniata; Hyperoartia; Myxiniiformes;
 OC Myxiniidae; Eptatretinae; Eptatretus.
 OX NCBI_TaxID=7764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded genes";
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).

Search completed: May 8, 2002, 11:48:28
Job time: 113 sec

CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AB025326; BAA8479.1; -.
DR HSSP: P56252; 1PDZ.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW glycolysis; lyase; Magnesium.
FT NON_TER 1
SQ SEQUENCE 395 AA; 43131 MW; D351C6700DC75CD CRC64;

Query Match 43.8%; Score 7; DB 13; Length 395;
Best Local Similarity 100.0%; Pred. No. 8.1;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 345 LVVGLCT 351

RESULT 15
ID 096656 PRELIMINARY; PRT; 434 AA.
AC 096656;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
DE "ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
OS Penaeus monodon (Penaeid shrimp).
OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
OC Penaeidae; Penaeus.
OX NCBI_TaxID=6687;
RN [1]
RP SEQUENCE FROM N.A.
RA TISSUE-ABDOMINAL MUSCLES;
RA Boonchouy C., Boonyawan B., Panyim S., Sonthayanon B.;
RT "Complete cDNA sequence of phosphopyruvate hydratase (enolase) from a marine shrimp, Penaeus monodon.";
RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2O).
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC EMBL: AF100985; AAC78141.1; -.
DR HSSP: P56252; 1PDZ.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW glycolysis; lyase; Magnesium; Pyruvate.
FT ACT_SITE 343 343 BY SIMILARITY.
FT METAL 355 355 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 434 AA; 47265 MW; EB575C6FB541ABD3 CRC64;

Query Match 43.8%; Score 7; DB 5; Length 434;
Best Local Similarity 100.0%; Pred. No. 8.8;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGLCT 7
|||||
DB 386 LVVGLCT 392

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:44:24 ; Search time 23.05 Seconds
(without alignments)
101.534 Million cell updates/sec

Title: US-09-647-457-2
Perfict score: 90
Sequence: 1 LVVGLCTCQIKTKGPAC 16

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 473505 seqs, 146272329 residues
Total number of hits satisfying chosen parameters: 473505

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :
1: SPREMBL_17:*
2: sp_archaea:*
3: sp_bacteria:*
4: sp_fungi:*
5: sp_human:*
6: sp_invertebrate:*
7: sp_mhc:*
8: sp_mammal:*
9: sp_oranella:*
10: sp_phage:*
11: sp_plant:*
12: sp_rodent:*
13: sp_virus:*
14: sp_vertebrate:*
14: sp_unclassified:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	65	72.2	154	4 Q9NPL4	Q9NPL4 homo sapien
2	65	72.2	159	5 Q9NG70	Q9NG70 peripatus s
3	65	72.2	272	4 Q9NPE2	Q9NPE2 homo sapien
4	65	72.2	353	11 Q9NKT7	Q9NKT7 mus musculu
5	65	72.2	383	5 Q9NG67	Q9NG67 tomocerus s
6	65	72.2	394	13 Q9PTX6	Q9PTX6 lampetra re
7	65	72.2	395	13 Q9PTX5	Q9PTX5 lampetra re
8	65	72.2	395	13 Q9USF7	Q9USF7 eplatretus
9	65	72.2	434	5 Q96556	Q96556 penaeus mon
10	65	72.2	434	13 Q9W7L2	Q9W7L2 sceloporus s
11	65	72.2	434	13 Q9W7L1	Q9W7L1 trachemys s
12	65	72.2	434	13 Q9W7L0	Q9W7L0 python regi
13	65	72.2	434	13 Q9PVK2	Q9PVK2 alligator m
14	58	64.4	251	5 Q9NG71	Q9NG71 limulus pol
15	55	61.1	159	5 Q9NG73	Q9NG73 eumecocampa
16	55	61.1	384	5 Q9NG68	Q9NG68 scolopendra
17	55	61.1	413	5 Q44100	Q44100 drosophila
18	55	61.1	413	5 Q44101	Q44101 drosophila
19	55	61.1	433	5 Q9VQ38	Q9VQ38 drosophila

20	53	58.9	433	3 Q93873	Q93873 pneumocysti
21	53	58.9	444	5 Q9BPL7	Q9BPL7 toxoplasma
22	51	56.7	326	10 Q42887	Q42887 lycopersico
23	51	56.7	444	10 Q9MA34	Q9MA34 lupinus lut
24	49	54.4	444	10 Q9LEB0	Q9LEB0 spinacia oi
25	48	53.3	162	5 Q9NG54	Q9NG54 spleonecte
26	48	53.3	385	5 Q9NG69	Q9NG69 polyxenys f
27	47.5	52.8	1664	5 Q9VQ2	Q9VQ2 caenorhabdi
28	47.5	52.8	2946	5 Q18857	Q18857 caenorhabdi
29	47	52.2	429	5 Q9N997	Q9N997 leishmania
30	47	52.2	439	5 Q9U615	Q9U615 mastigamoeb
31	47	52.2	446	5 Q9UAL5	Q9UAL5 plasmodium
32	46	51.1	137	10 Q9T0P1	Q9T0P1 triticum ae
33	46	51.1	137	10 Q9S9D7	Q9S9D7 hordeum vul
34	46	51.1	1477	10 Q9SC94	Q9SC94 arabidopsis
35	45.5	50.6	317	13 Q9MBD0	Q9MBD0 brachydanio
36	45.5	50.6	318	13 Q9B0K2	Q9B0K2 brachydanio
37	45	50.0	90	10 Q9S6Y2	Q9S6Y2 triticum ae
38	45	50.0	234	10 Q9ATU6	Q9ATU6 arabidopsis
39	45	50.0	396	12 Q9YK89	Q9YK89 rubella vir
40	44	48.9	43	4 Q99225	Q99225 homo sapien
41	44	48.9	427	4 Q9H152	Q9H152 homo sapien
42	44	48.9	678	4 Q9Y6P2	Q9Y6P2 homo sapien
43	43	47.8	85	2 Q07207	Q07207 mycobacteri
44	43	47.8	429	5 Q9NDH8	Q9NDH8 trypanosoma
45	43	47.8	444	5 Q9UAE6	Q9UAE6 toxoplasma

ALIGNMENTS

RESULT	ID	Q9NPL4	PRELIMINARY:	PRT:	154 AA.
AC	Q9NPL4	Q9NPL4			
DT	01-OCT-2000	(TREMBLrel. 15, Created)			
DT	01-OCT-2000	(TREMBLrel. 15, Last sequence update)			
DT	01-JUN-2001	(TREMBLrel. 17, Last annotation update)			
DE	ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA	Andreu N., Estivill X., Escarceller M., Sunoy L.;				
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RA	Auffray C., Ansoyge W., Ballabio A., Estivill X., Gibson K.,				
RA	Lehrach H., Pousotka A., Lundeberg J.;				
RT	"The European IMAGE consortium for Integrated Molecular analysis of				
RT	human gene transcripts.";				
RL	Submitted (JUN-2000) to the EMBL/Genbank/DBJ databases.				
CC	-1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H2O.				
CC	-1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING				
CC	THE DIMER (BY SIMILARITY).				
CC	-1- PATHWAY: GLYCOLYSIS.				
CC	-1- SUBUNIT: HOMODIMER (BY SIMILARITY).				
CC	-1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).				
CC	-1- SIMILARITY: TO THE ENOLASE FAMILY.				
DR	EMBL: AL359213; CAB94588.1; -.				
DR	InterPro: IPR000941; Enolase.				
DR	Pfam: PF00113; enolase; 1.				
DR	PRINTS: PR00148; ENOLASE.				
DR	Prodom: PD000902; Enolase; 1.				
DR	PROSITE: PS00164; ENOLASE; 1.				
KW	Glycolysis; Lyase; Magnesium.				
FT	NOV_TER				
SQ	SEQUENCE	154 AA;	16937 MW;	347B95809B1C664D	CRC64;

Query Match 72.2%; Score 65; DB 4; Length 154;
Best Local Similarity 81.2%; Pred. No. 0.00061;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 104 LVVGLCTGQIKTGAPC 119

RESULT 2

O9NG670 PRELIMINARY; PRT; 159 AA.

AC 09NG670;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Peripatus sp. 'Per3'.
OC Eukaryota; Metazoa; Onychophora; Peripatidae; Peripatus.
OX NCBI_TaxID=126380;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PER3248_407;
RA Regier J.C., Shultz J.W.;
RT "Enolase as a phylogenetic marker."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF258667; AAF72638.1; -.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRODOM: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW GLYCOLYSIS; Lyase; Magnesium.
FT NON_TER 1
FT NON_TER 159
SQ SEQUENCE 159 AA; 17582 MW; 840E266ACD36D3CD CRC64;

Query Match 72.2%; Score 65; DB 5; Length 159;
Best Local Similarity 81.2%; Pred. No. 0.00063;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 138 LVVGLCTGQIKTGAPC 153

RESULT 3

O9BT62 PRELIMINARY; PRT; 272 AA.

AC 09BT62;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
UNKNOWN (PROTEIN FOR IMAGE:3629132) (FRAGMENT).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=CHORIOCARCINOMA;
RA Strausberg R.;

RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004325; AA04325.1; -.
FT NON_TER 1
SQ SEQUENCE 272 AA; 29883 MW; 08F1755ADEA8BD0C CRC64;

Query Match 72.2%; Score 65; DB 4; Length 272;
Best Local Similarity 81.2%; Pred. No. 0.00098;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 222 LVVGLCTGQIKTGAPC 237

RESULT 4

O99KT7 PRELIMINARY; PRT; 353 AA.

AC 099KT7;
DT 01-JUN-2001 (TREMBLrel. 17, Created)
DT 01-JUN-2001 (TREMBLrel. 17, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
SIMILAR TO ENOLASE 1, ALPHA NON-NEURON (FRAGMENT).
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA Strausberg R.;
RT Submitted (FEB-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL: BC004017; AA04017.1; -.
FT NON_TER 1
FT NON_TER 353
SQ SEQUENCE 353 AA; 38299 MW; 2DBD375CE1C26A43 CRC64;

Query Match 72.2%; Score 65; DB 11; Length 353;
Best Local Similarity 81.2%; Pred. No. 0.0012;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 303 LVVGLCTGQIKTGAPC 318

RESULT 5

O9NG67 PRELIMINARY; PRT; 383 AA.

AC 09NG67;
DT 01-OCT-2000 (TREMBLrel. 15, Created)
DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
DE 01-JUN-2001 (TREMBLrel. 17, last annotation update)
ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Tomocerus sp. 'Tom'.
OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Collembola; Arthropoleona; Entomobryoidae; Tomoceridae; Tomocerus.
OX NCBI_TaxID=111305;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=TM23_406;
RA Regier J.C., Shultz J.W.;
RT "Enolase as a phylogenetic marker."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSHOENOLPYRUVATE + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
DR EMBL: AF258670; AAF72641.1; -.

DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase: 1.
 DR PROSITE: PS00164; ENOLASE: 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 383
 SQ SEQUENCE 383 AA; 41326 MW; 4523F005F6A5E579 CRC64;

Query Match 72.2%; Score 65; DB 5; Length 383;
 Best Local Similarity 81.2%; Pred. NO. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
 Db 363 LVVGLCTGQIKTGAPC 378

RESULT 6

Q9PTX6 PRELIMINARY; PRT; 394 AA.
 AC Q9PTX6; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 GN ENOLASE-1.
 OS Lampetia reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_Taxid=7753;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded RT genes."
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 DR EMBL: AB025330; BAA88483.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase: 1.
 DR PROSITE: PS00164; ENOLASE: 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 394
 SQ SEQUENCE 394 AA; 42583 MW; BC585FE6C712A3D2 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 394;
 Best Local Similarity 81.2%; Pred. NO. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
 Db 345 LVVGLCTGQIKTGAPC 360

RESULT 7
 Q9PTX5 PRELIMINARY; PRT; 395 AA.

AC Q9PTX5; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 GN ENOLASE-2.
 OS Lampetia reissneri.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Hyperoartia;
 OC Petromyzontiformes; Petromyzontidae; Lampetra.
 OX NCBI_Taxid=7753;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded RT genes."
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 DR EMBL: AB025330; BAA88483.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase: 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase: 1.
 DR PROSITE: PS00164; ENOLASE: 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1
 FT NON_TER 395
 SQ SEQUENCE 395 AA; 43266 MW; 8591D6862DA8544 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 395;
 Best Local Similarity 81.2%; Pred. NO. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
 Db 345 LVVGLCTGQIKTGAPC 360

RESULT 8

Q9USE7 PRELIMINARY; PRT; 395 AA.
 AC Q9USE7; 01-MAY-2000 (Tremblrel. 13, Created)
 DT 01-MAY-2000 (Tremblrel. 13, last sequence update)
 DT 01-JUN-2001 (Tremblrel. 17, last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Epiplatys burgeri (Inshore hagfish).
 OC Eukaryota; Metazoa; Chordata; Craniata; Hyperotreti; Myxiniiformes;
 OC Myxiniidae; Epiplatinae; Epiplatelus.
 OX NCBI_Taxid=7764;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20063780; PubMed=10594174;
 RA Kuraku S., Hoshiyama D., Katoh K., Suga H., Miyata T.;
 RT "Monophyly of lampreys and hagfishes supported by nuclear DNA-coded RT genes."
 RL J. Mol. Evol. 49:729-735(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.

CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AB025326; BAA8479.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DR GLYCOLYSIS: Lyase; Magnesium.
 FT NON_TER 1
 SQ SEQUENCE 395 AA; 43131 MW; D351C670DDC75CD CRC64;

Query Match 72.2%; Score 65; DB 13; Length 395;
 Best Local Similarity 81.2%; Pred. No. 0.0013;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
 ||||| |||||
 Db 345 LVVGLCTGQIKTGAPC 360

RESULT 9
 ID 096656 PRELIMINARY; PRT; 434 AA.
 AC 096656;
 DT 01-MAY-1999 (TREMBLrel. 10, Created)
 DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OS Penaeus monodon (Penaeid shrimp).
 OC Eukaryota; Metazoa; Arthropoda; Crustacea; Malacostraca;
 OC Eumalacostraca; Eucarida; Decapoda; Dendrobranchiata; Penaeoidea;
 OC Penaeidae; Penaeus.
 OX NCBI_TaxID=6687;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=ABDOMINAL MUSCLES;
 RA Boonhoun C., Boonyawan B., Panyim S., Sonthayanon B.;
 RT "Complete cDNA sequence of phosphopyruvate hydratase (enolase) from a marine shrimp, Penaeus monodon."
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF100985; AAC78141.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DE GLYCOLYSIS: Lyase; Magnesium.
 DE ACT_SITE 343 BY SIMILARITY.
 FT METAL 355 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 434 AA; 47265 MW; EB575C6FB541ABD3 CRC64;

Query Match 72.2%; Score 65; DB 5; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
 ||||| |||||
 Db 386 LVVGLCTGQIKTGAPC 401

RESULT 10
 ID 09W7L2 PRELIMINARY; PRT; 434 AA.
 AC 09W7L2;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OS Sceloporus undulatus (Eastern fence lizard).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Lepidosauria; Squamata; Iguania; Iguanidae; Phrynosomatinae;
 OC Sceloporus.
 OX NCBI_TaxID=8520;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC EMBL: AF072587; AAD41644.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR PRODOM: PD000902; ENOLASE; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 DE GLYCOLYSIS: Lyase; Magnesium.
 FT ACT_SITE 341 BY SIMILARITY.
 FT METAL 353 MAGNESIUM (BY SIMILARITY).
 SQ SEQUENCE 434 AA; 47493 MW; 6E377E0F0A767E11 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
 ||||| |||||
 Db 384 LVVGLCTGQIKTGAPC 399

RESULT 11
 ID 09W7L1 PRELIMINARY; PRT; 434 AA.
 AC 09W7L1;
 DT 01-NOV-1999 (TREMBLrel. 12, Created)
 DT 01-NOV-1999 (TREMBLrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ALPHA ENOLASE (EC 4.2.1.11).
 OS Trachemys scripta elegans.
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Testudines; Cryptodira; Testudinoidae; Emydidae; Trachemys.
 OX NCBI_TaxID=31138;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.

DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR Prodom: PD000902; Enolase; 1.
 KW Lyase.
 SQ SEQUENCE 434 AA; 47333 MW; 1AF6D392C539DD16 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LVVGLCTCQIKTGAPC 16
 Db 384 LVVGLCTCQIKTGAPC 399

RESULT 12
 09W710 PRELIMINARY; PRT; 434 AA.
 AC 09W710;
 DT 01-NOV-1999 (TREMblrel. 12, Created)
 DT 01-NOV-1999 (TREMblrel. 12, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Lepidodonta; Squamata; Scleroglossa; Serpentes; Boidae; Pythonidae; OC Python.
 OX NCBI_TaxID=51751;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF072589; AAD41646.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR Prodom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT ACT_SITE 341
 FT METAL 353
 FT METAL 353
 SQ SEQUENCE 434 AA; 47570 MW; F242F93B6D467033 CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LVVGLCTCQIKTGAPC 16
 Db 384 LVVGLCTCQIKTGAPC 399

RESULT 13
 09PVK2 PRELIMINARY; PRT; 434 AA.
 AC 09PVK2;
 DT 01-MAY-2000 (TREMblrel. 13, Created)
 DT 01-MAY-2000 (TREMblrel. 13, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)

DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE).
 OS Alligator mississippiensis (American alligator).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Archosauria; Crocodylia; Alligatorinae; Alligator.
 OX NCBI_TaxID=8496;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=MUSCLE;
 RX MEDLINE-99439677; PubMed=10508547;
 RA Mannen H., Li S.S.-L.;
 RT "Molecular evidence for a clade of turtles."
 RL Mol. Phylogenet. Evol. 13:144-148(1999).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF072586; AAD41643.1; -.
 DR HSSP: P56252; 1PDZ.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR Prodom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 SQ SEQUENCE 434 AA; 47322 MW; DFD23524BECF5ECA CRC64;

Query Match 72.2%; Score 65; DB 13; Length 434;
 Best Local Similarity 81.2%; Pred. No. 0.0014;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 Oy 1 LVVGLCTCQIKTGAPC 16
 Db 384 LVVGLCTCQIKTGAPC 399

RESULT 14
 09NG71 PRELIMINARY; PRT; 251 AA.
 ID 09NG71;
 AC 09NG71;
 DT 01-OCT-2000 (TREMblrel. 15, Created)
 DT 01-OCT-2000 (TREMblrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMblrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Limulus polyphemus (Atlantic horseshoe crab).
 OC Eukaryota; Metazoa; Arthropoda; Chelicerata; Merostomata; Xiphosura;
 OX Limulidae; Limulus.
 OX NCBI_TaxID=6850;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=LPO156.406;
 RA Regier J.C., Shultz J.W.;
 RT "Enolase as a phylogenetic marker."
 RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2O).
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL: AF258666; AAF72637.2; -.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR Prodom: PD000902; Enolase; 1.

DR PROSITE: PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1 1
 FT NON_TER 251 1
 SQ SEQUENCE 251 AA; 27452 MW; DEE7B1BA7A87693F CRC64;

Query Match 64.4%; Score 58; DB 5; Length 251;
 Best Local Similarity 92.3%; Pred. No. 0.016;
 Matches 12; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTG 13
 |||||
 DB 230 LVVGLCTCQIKTG 242

RESULT 15

Q9NG73 PRELIMINARY; PRT; 159 AA.
 AC Q9NG73;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-JUN-2001 (TREMBLrel. 17, Last annotation update)
 DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
 OS Eumesocampa frigidilis.
 OC Eukaryota; Metazoa; Arthropoda; Tracheata; Hexapoda; Diplura; Campodeidae; Eumesocampa.
 OX NCBI_TaxID=109745;
 RN [1]
 RP -SEQUENCE FROM N.A.
 RC STRAIN=EF248_407;
 RA Reiter J.C., Shultz J.W.;
 RL Submitted (Apr-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING THE DIMER (BY SIMILARITY).
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
 CC -1- SIMILARITY: TO THE ENOLASE FAMILY.
 DR EMBL; AF258664; AAF72635.1; -.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS; PR00148; ENOLASE.
 DR PRODOM; PD000902; ENOLASE; 1.
 DR PROSITE; PS00164; ENOLASE; 1.
 KW Glycolysis; Lyase; Magnesium.
 FT NON_TER 1 1
 FT NON_TER 159 159
 SQ SEQUENCE 159 AA; 17547 MW; 448E41A6DF664D0 CRC64;

Query Match 61.1%; Score 55; DB 5; Length 159;
 Best Local Similarity 75.0%; Pred. No. 0.037;
 Matches 12; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTG 16
 |||||
 DB 138 LVVGLSTGQIKTGAPC 153

Search completed: May 8, 2002, 11:46:16
 Job time: 112 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:44:44 ; Search time 10.17 Seconds

(without alignments)
57.683 Million cell updates/sec

Title: US-09-647-457-2

Perfect score: 90

Sequence: 1 LVVGLTCQIKTGPAC 16

Scoring table: BLOSUM62

Searched: 100059 seqs, 36664827 residues

Total number of hits satisfying chosen parameters: 100059

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_39.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,

and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	74	82.2	458	1 ENOL_HUMAN	Q05524 homo sapien
2	68	75.6	433	1 ENOA_BOVIN	Q9KJ44 bos taurus
3	65	72.2	395	1 ENO_ALBAT	P42897 alligator m
4	65	72.2	433	1 ENOA_ANAPL	P19140 anas platyr
5	65	72.2	433	1 ENOA_CHICK	P51913 gallus gall
6	65	72.2	433	1 ENOA_HUMAN	P06733 homo sapien
7	65	72.2	433	1 ENOA_MOUSE	P17182 mus musculu
8	65	72.2	433	1 ENOA_RAT	P07322 ratu
9	65	72.2	433	1 ENOB_CHICK	P13929 homo sapien
10	65	72.2	433	1 ENOB_HUMAN	P21550 mus musculu
11	65	72.2	433	1 ENOB_MOUSE	P25704 onychomys
12	65	72.2	433	1 ENOB_RABIT	P15429 ratu
13	65	72.2	433	1 ENOB_RAT	P09104 homo sapien
14	65	72.2	433	1 ENOG_HUMAN	P17183 mus musculu
15	65	72.2	433	1 ENOG_MOUSE	P07323 ratu
16	65	72.2	433	1 ENOG_RAT	P56252 homariu gam
17	65	72.2	433	1 ENO_HOMGA	P08734 xenopus lae
18	65	72.2	433	1 ENO_XENLA	P08734 xenopus lae
19	65	72.2	433	1 ENO_LOLPE	P08734 xenopus lae
20	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
21	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
22	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
23	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
24	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
25	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
26	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
27	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
28	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
29	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
30	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
31	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
32	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae
33	65	72.2	433	1 ENO_SCHJA	P08734 xenopus lae

34	50	55.6	445	1 ENO_RITCO	P42896 ricinus com
35	49	54.4	436	1 ENO_NEOFR	P42894 neocallima
36	49	54.4	444	1 ENO_MESCR	Q43130 mesembryant
37	49	54.4	446	1 ENO1_MAIZE	P26301 zea mays (m
38	48	53.3	372	1 ENO1_CHIRE	P16883 chlamydomon
39	47	52.2	436	1 ENO1_ENTHI	P1555 entamoeba h
40	47	52.2	446	1 ENO1_PLAFA	Q27727 plasmodium
41	46.5	51.7	436	1 ENO1_YEAST	P00924 saccharomyc
42	46.5	51.7	436	1 ENO2_YEAST	P00925 saccharomyc
43	46	51.1	126	1 THN1_WHEAT	P01544 triticum ae
44	46	51.1	137	1 THN3_WHEAT	P08772 hordeum vul
45	46	51.1	137	1 THN6_HORVU	P09618 hordeum vul

ALIGNMENTS

RESULT 1
ID ENOL_HUMAN STANDARD: PRT; 458 AA.

AC Q05524;
DT 01-FEB-1995 (Rel. 31, Created)
DT 01-FEB-1995 (Rel. 31, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE, LUNG SPECIFIC (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE
DE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
GN ENO1B.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_Taxid=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX TISSUE=Lung fibroblast;
RX MEDLINE=93372640; PubMed=7689884;
RA Verma M., Kurl R.N.;
RT "Human lung enolase: cloning and sequencing of cDNA and its
RT inducibility with dexamethasone."
RL Biochem. Mol. Biol. Int. 30:293-303(1993).

CC -1 CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2O).
CC -1 COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC -1 PATHWAY: GLYCOLYSIS.
CC -1 SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1 SUBCELLULAR LOCATION: CYTOPLASMIC (POTENTIAL).
CC -1 INDUCTION: BY DEXAMETHASONE.
CC -1 SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC EMBL: X66610; CAA47179.1; -
DR HSSP; P56252; IPDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; ENOLASE; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium; Multigene family.
FT ACT_SITE 167 167
FT METAL 254 254
FT METAL 308 308
FT METAL 336 336
SQ SEQUENCE 458 AA; 49477 MW; 2550F34A2BF44314 CRC64;

Query Match 82.2%; Score 74; DB 1; Length 458;

Best Local Similarity 87.5%; Pred. No. 0.00018;
Matches 14; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 407 LVVGLCTGQIKTGAPC 422

RESULT 2

ENO_A_BOVIN STANDARD; PRT; 433 AA.
AC Q9X5J4;
DT 20-AUG-2001 (Rel. 40, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-NEURAL ENOLASE) (NNE) (PHOSPHOPRUVATE HYDRALYASE).
GN ENO1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RA Chapman K.L., Newman B., Hillaby M.C., Freemont A.J., Grant M.E.,
RA Boot-Handford R., Wallis G.A.;
RT "Alpha enolase is upregulated in proliferative chondrocytes in the
epiphyseal growth plate and in human osteoarthritic tissue."
RL Submitted (May-1999) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC (BY SIMILARITY).
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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or send an email to license@isb-sib.ch).
CC -----
CC EMBL: AF149256; AAD33073.1; -.
CC DR HSSP: P56252; 1PDZ.
CC DR InterPro: IPR000941; Enolase.
CC DR Pfam: PF00113; enolase; 1.
CC DR PRINTS: PR00146; ENOLASE.
CC KW Lyase; Glycolysis; Magnesium; Multigene family.
CC FT INIT_MET 0
CC FT ACT_SITE 157 157 BY SIMILARITY.
CC FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SQ SEQUENCE 433 AA; 47145 MW; B004E95C46F2E0C CRC64;

Query Match 75.6%; Score 68; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0015;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 3

ENO_ALLMI STANDARD; PRT; 395 AA.

AC P42697;
DT 01-NOV-1995 (Rel. 32, Created)
DT 01-NOV-1995 (Rel. 32, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ENOLASE (EC 4.2.1.11) (2-PHOSPHOGLYCERATE DEHYDRATASE) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (FRAGMENT).
OS Alligator mississippiensis (American alligator).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Crocodylidae; Alligatorinae; Alligator.
OX NCBI_TaxID=8496;
RN [1]
RP MEDLINE=94195794; PubMed=8146164;
RX Hedge S.B.,
RT "Molecular evidence for the origin of birds";
RL Proc. Natl. Acad. Sci. U.S.A. 91:2621-2624(1994).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.

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CC -----
CC EMBL: L28078; AA53671.1; -.
CC DR HSSP: P56252; 1PDY.
CC DR InterPro: IPR000941; Enolase.
CC DR Pfam: PF00113; enolase; 1.
CC DR ProDom: PD000902; Enolase; 1.
CC DR PROSITE: PS00164; ENOLASE; 1.
CC KW Lyase; Glycolysis; Magnesium.
CC FT NON_TER 1
CC FT ACT_SITE 136 136 BY SIMILARITY.
CC FT METAL 223 223 MAGNESIUM (BY SIMILARITY).
CC FT METAL 271 271 MAGNESIUM (BY SIMILARITY).
CC FT METAL 296 296 MAGNESIUM (BY SIMILARITY).
CC FT NON_TER 395
CC SQ SEQUENCE 395 AA; 42884 MW; B43E91228E9110B5 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 395;
Best Local Similarity 81.2%; Pred. No. 0.004;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVVGLCTGQIKTGAPC 16
DB 362 LVVGLCTGQIKTGAPC 377

RESULT 4

ENO_A_NAPL STANDARD; PRT; 433 AA.

AC P19140;
DT 01-NOV-1990 (Rel. 16, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (TAU-CRYSTALLIN).
OS Anas platyrhynchos (Domestic duck).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

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OC Archosauria; Aves; Neognathae; Anseriformes; Anatidae; Anas.
OX NCBI_TaxID=8839;
RN [1]
RC SEQUENCE FROM N.A.
RX MEDLINE=89079778; PubMed=2462567;
RA Wistow G.J., Lietman T., Williams L.A., Stapel S.O., de Jong W.W.,
RT Horwitz J., Piatigorsky J.;
RT "tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a
RT lens structural protein."
RL J. Cell Biol. 107:2729-2736(1988).
CC -1- FUNCTION: BOTH AN ENZYME AND A LENS STRUCTURAL PROTEIN.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M0749; AAA9218.1; -
DR EMBL: X14195; CA32409.1; -
DR PIR: A32132; A32132.
DR HSP: P56252; 1PDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; ENOLASE.1.
DR PROSITE: PS00164; ENOLASE.1.
KW -Lyase; Glycolysis; Magnesium; Eye lens protein.
FT INIT MET 0
FT ACT SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 433 AA; 47108 MW; 1AED7B08A66E84D CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 5
ENOA_CHICK STANDARD; PRT; 433 AA.
ID ENOA_CHICK
AC P51913;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (PHOSPHOPYRUVATE HYDRATASE).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=WHITE LEGHORN; TISSUE=Kidney;

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RX MEDLINE=95355305; PubMed=7629021;
RA Tanaka M., Maeda K., Nakashima K.;
RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent
RT tyrosine-phosphorylation site: cDNA cloning and nucleotide sequence
RT analysis."
RL J. Biochem. 117:554-559(1995).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER (BY SIMILARITY).
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER (BY SIMILARITY).
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D37900; BA07132.1; -
DR HSP: P56252; 1PDY.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; ENOLASE.1.
DR PROSITE: PS00164; ENOLASE.1.
KW Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT MET 0
FT ACT SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
SQ SEQUENCE 433 AA; 47173 MW; 93AD6B0A7AD99910 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 6
ENOA_HUMAN STANDARD; PRT; 433 AA.
ID ENOA_HUMAN
AC P06733; Q16704; Q90M55;
DT 01-JAN-1988 (Rel. 06, Created)
DT 01-APR-1988 (Rel. 07, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
DE NEURAL ENOLASE) (NNE) (PHOSPHOPYRUVATE HYDRATASE).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=86313654; PubMed=3529090;
RA Galliongo A., Feo S., Moore R., Croce C.M., Shove L.C.;
RT "Molecular cloning and nucleotide sequence of a full-length cDNA for
RT human alpha enolase."
RL Proc. Natl. Acad. Sci. U.S.A. 83:6741-6745(1986).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=90323004; PubMed=2373081;
RA Galliongo A., Oliva D., Cali L., Barba G., Barbieri G., Feo S.;

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RT "Structure of the human gene for alpha-enolase.";
RL Eur. J. Biochem. 190:567-573(1990).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Endometrium; PubMed=8824716;
RX MEDLINE=9642209; PubMed=8824716;
RA Walter M., Leidenberger F.A., Scheppe K.W., Northmann W.;
RT "Autoreactive epitopes within the human alpha-enolase and their
RL recognition by sera from patients with endometriosis.";
RN J. Autoimmun. 8:937-945(1995).
RN [4]
RP SEQUENCE OF 165-433 FROM N.A.
RX MEDLINE=98317532; PubMed=9653645;
RA Onyango P., Luboyva B., Gardellin P., Kurzbauer R., Welch A.;
RT "Molecular cloning and expression analysis of five novel genes in
RL chromosome 1p36.";
RN Genomics 50:187-198(1998).
RN [5]
RP SEQUENCE OF 269-280 AND 306-320.
RX MEDLINE=95307697; PubMed=7787969;
RA Mohamed R.M., Handan M.Y., Maki A., Al-Katib A.;
RT "Induced expression of alpha-enolase in differentiated diffuse large
RL cell lymphoma.";
RN Enzyme Protein 48:37-44(1995).
RN [6]
RP SEQUENCE OF 1-8.
RX TISSUE=Colon carcinoma; PubMed=9150948;
RA MEDLINE=97295306; PubMed=9150948;
RT "A two-dimensional gel database of human colon carcinoma proteins.";
RL Electrophoresis 18:605-613(1997).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL: M14328; AAA52387.1; -
DR EMBL: X16288; CAA34360.1; -
DR EMBL: X16289; CAA34360.1; JOINED.
DR EMBL: X16290; CAA34360.1; JOINED.
DR EMBL: X84907; CAA59331.1; -
DR EMBL: U88968; AAC39935.1; -
DR PIR: A29170; A29170.
DR PIR: S11696; S11696.
DR HSSP: P56252; 1PDY.
DR Aarhus/Shent-2DPAGE; 1325; IEF.
DR Aarhus/Shent-2DPAGE; 5406; NEPHEGE.
DR MIM: 172430; -
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase.1.
DR PRINTS: PR00148; ENOLASE.
DR PRODOM: PD000902; ENOLASE.1.
DR PROSITE: PS00164; ENOLASE.1.
KW lysase; Glycolysis; Magnesium; Multigene family.
FT INIT MET 0 0
FT ACT_SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).

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FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 251 251 F -> S (IN REF. 3).
SO SEQUENCE 433 AA; 47037 MW; B2028684C33140B5 CRC64;

Query Match
Best Local Similarity 72.2%; Score 65; DB 1; Length 433;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

OY 1 LVGLCTQIKTGAPC 16
Db 383 LVGLCTQIKTGAPC 398

RESULT 7
ENOA_MOUSE STANDARD: PRT: 433 AA.
ID ENOA_MOUSE
AC P17182; Q9DCY7;
DT 01-AUG-1990 (Rel. 15, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
DE NEURAL ENOLASE) (NNE).
GN ENOI OR ENO-1.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_Taxid=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=90301487; PubMed=2362815;
RA Kaghad M., Dumont X., Chalon P., Lelias J.M., Lamané N., Lucas M.,
RA Lazar M., Caput D.;
RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from
RL mouse brain.";
RN Nucleic Acids Res. 18:3638-3638(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=Kidney;
RX MEDLINE=21085660; PubMed=11217851;
RA Kawai J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
RA Arikawa T., Hara A., Fukunishi Y., Kono H., Adachi J., Fukuda S.,
RA Aizawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamamaki I.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Kadota K., Matsuda H.A., Ashburner M., Batalov S., Casavant T.,
RA Fletschmann W., Gaasterland T., Gissi C., King B., Kochava H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Gustincich S., Hill D., Hofmann M., Hume D.A., Kamuya M., Lee N.H.,
RA Lyons P., Marchionni L., Mashima J., Mazzaletti J., Kombearts P.,
RA Nordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
RA Suzuki H., Toyooka K., Wang K.H., Weltz C., Whitaker C., Wilming L.,
RA Wyszynski B., Yoshida K., Hasegawa Y., Kawai H., Kohsaki S.,
RA Hayashizaki Y.;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.

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CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X52379; CAA36605.1; -
CC EMBL: AK002336; BAB22021.1; -
CC PIR: S10246; S10246.
CC HSSP: P56252; 1PDY.
CC SWISS-2DPAGE: P17182; MOUSE.
CC MGD: MGI:95393; Enol.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE.1.
CC PROSITE: PS00164; ENOLASE.1.
CC KMWase: Glycolysis; Magnesium; Multigene family.
CC LYT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC CONFLICT 358 358 L -> P (IN REF. 1).
CC SEQUENCE 433 AA; 47009 MW; C90082CBA8290EB6 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 8
ENOA_RAT STANDARD; PRT; 433 AA.
AC P04764;
DT 13-AUG-1987 (Rel. 05, Created)
DT 13-AUG-1987 (Rel. 05, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE ALPHA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE) (NON-
DE NEURAL ENOLASE) (NNE).
GN ENOI OR ENO-1.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RA MEDLINE=85242108; PubMed=2989793;
RA Sakimura K., Kushiya E., Obinata M., Takahashi Y.;
RT "Molecular cloning and the nucleotide sequence of cDNA to mRNA for
RT non-neuronal enolase (alpha alpha enolase) of rat brain and liver.";
RL Nucleic Acids Res. 13:4365-4378(1985).
RN [2]
RP SEQUENCE FROM N.A.
RA Takahashi Y.;
RA Submitted (JAN-1986) to the EMBL/GenBank/DBJ databases.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN

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CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: X02610; CAA26456.1; -
CC PIR: A23126; A23126.
CC HSSP: P56252; 1PDY.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase.1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE.1.
CC PROSITE: PS00164; ENOLASE.1.
CC KMWase: Glycolysis; Magnesium; Multigene family.
CC LYT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 433 AA; 46984 MW; F1A25F010C276E7C CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

RESULT 9
ENOB_CHICK STANDARD; PRT; 433 AA.
AC P07322;
DT 01-APR-1988 (Rel. 07, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (PHOSPHOPYRUVATE HYDRATASE).
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=WHITE LEGHORN; TISSUE=Muscle;
RX MEDLINE=95355305; PubMed=7629021;
RA Tanaka M., Maeda K., Nakashima K.;
RT "Chicken alpha-enolase but not beta-enolase has a Src-dependent
RT lysosine-phosphorylation site: cDNA cloning and nucleotide sequence
RT analysis.";
RL Biochem. J. 236:115-126(1986).
RN [2]
RP SEQUENCE.
RA MEDLINE=87075592; PubMed=3539098;
RA Russell G.A., Dunbar B., Fothergill-Gilmore L.A.;
RT "The complete amino acid sequence of chicken skeletal muscle
RT enolase.";
RL Biochem. J. 236:115-126(1986).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.

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CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D37901; BAA07133.1; -.
DR PIR: A23850; A23850.
DR HSP: P56252; 1PDX.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KM Lyase; Glycolysis; Magnesium; Multigene family; Acetylation.
FT INIT_MET 0 0
FT MOD_RES 1 1
FT ACT_SITE 157 157 ACETYLATION.
FT METAL 244 244 BY SIMILARITY.
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 16 16 E -> D (IN REF. 2).
FT CONFLICT 48 48 P -> L (IN REF. 2).
FT CONFLICT 93 93 M -> V (IN REF. 2).
FT CONFLICT 118 119 CK -> SH (IN REF. 2).
FT CONFLICT 208 208 G -> D (IN REF. 2).
FT CONFLICT 257 257 H -> D (IN REF. 2).
FT CONFLICT 265 266 HT -> DP (IN REF. 2).
FT CONFLICT 269 269 Y -> L (IN REF. 2).
FT CONFLICT 308 308 F -> S (IN REF. 2).
FT CONFLICT 322 322 T -> A (IN REF. 2).
FT CONFLICT 330 330 G -> A (IN REF. 2).
FT CONFLICT 342 342 K -> G (IN REF. 2).
FT CONFLICT 393 394 KT -> EO (IN REF. 2).
SQ SEQUENCE 433 AA; 47065 MW; 9BC2FB5FB910C254 CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTQIKTGAPC 16
DB 383 LVVGLCTQIKTGAPC 398

RESULT 10
ID ENOB_HUMAN STANDARD; PRT; 433 AA.
AC P13929;
DT 01-JAN-1990 (Rel. 13, Created)
DT 01-OCT-1993 (Rel. 27, Last sequence update)
DT 20-ANG-2001 (Rel. 40, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PROSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE) (MSE).
GN ENO3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
OC NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=90067857; Pubmed=2587223;
RA Peshavaria M., Hinks L.J., Day I.N.M.;
RT "Structure of human muscle (beta) enolase mRNA and protein deduced
RT from a genomic clone.";

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RL Nucleic Acids Res. 17:8862-8862(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=91222137; Pubmed=1840492;
RA Peshavaria M., Day I.N.M.;
RT "Molecular structure of the human muscle-specific enolase gene
RT (ENO3).";
RL Biochem. J. 275:427-433(1991).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=90245587; Pubmed=2336366;
RA Cali L., Feo S., Oliva D., Giallongo A.;
RT "Nucleotide sequence of a cDNA encoding the human muscle-specific
RT enolase (MSE).";
RL Nucleic Acids Res. 18:1893-1893(1990).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=93292497; Pubmed=8513787;
RA Giallongo A., Venturella S., Oliva D., Barbieri G., Rubino P.,
RA Feo S.;
RT "Structural features of the human gene for muscle-specific enolase.
RT Differential splicing in the 5'-untranslated sequence generates two
RT forms of mRNA.";
RL Eur. J. Biochem. 214:367-374(1993).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL: X16504; CAA34513.1; -.
DR EMBL: X51957; CAA36216.1; -.
DR EMBL: X55976; CAA39446.1; -.
DR EMBL: X56832; CAA40163.1; -.
DR PIR: S15933; S15933.
DR PIR: S06756; S06756.
DR PIR: S14759; S14759.
DR PIR: S31650; S31650.
DR PIR: S33330; S33330.
DR HSP: P56252; 1PDX.
DR MIM: 131370; -.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KM Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT_MET 0 0
FT ACT_SITE 157 157 BY SIMILARITY.
FT METAL 244 244 MAGNESIUM (BY SIMILARITY).
FT METAL 292 292 MAGNESIUM (BY SIMILARITY).
FT METAL 317 317 MAGNESIUM (BY SIMILARITY).
FT CONFLICT 84 84 V -> A (IN REF. 3).
FT CONFLICT 161 161 K -> N (IN REF. 1 AND 2).
SQ SEQUENCE 433 AA; 46855 MW; 5F726D743DBFB2F CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;

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Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 11
ENOB_MOUSE
ID ENOB_MOUSE STANDARD: PRT: 433 AA.
AC P21550;
DT 01-MAY-1991 (Rel. 18, Created)
DT 01-AUG-1992 (Rel. 23, Last sequence update)
DT 15-JUL-1999 (Rel. 38, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
GN ENO3 OR ENO-3.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=BAIB/C; TISSUE=Liver;
RA Lamande N., Brosset S., Keller A., Lucas M., Lazar M.;
RL Submitted (SEP-1991) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C3H;
RA MEDLINE=92290133; PubMed=1339335;
RA Peterson C.A., Cho M., Rastinejad F., Blau H.M.;
RT "Beta-enolase is a marker of human myoblast heterogeneity prior to
differentiation.";
RL Dev. Biol. 151:626-629(1992).
RN [3]
RP SEQUENCE OF 58-433 FROM N.A.
RA MEDLINE=89282789; PubMed=2734297;
RA Lamande N., Mazo A.M., Lucas M., Montarras D., Pinset C., Gros F.,
RA Legault-Demare L., Lazar M.;
RT "Murine muscle-specific enolase: cDNA cloning, sequence, and
developmental expression.";
RL Proc. Natl. Acad. Sci. U.S.A. 86:4445-4449(1989).
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----
DR EMBL; X61600; CAA43797.1; -;
DR EMBL; X62667; CAA44540.1; -;
DR EMBL; M20745; AAA37554.1; -;
DR EMBL; X57747; CAA40913.1; -;
DR PIR; S17109; NOKSB.
DR PIR; A33921; A33921.
DR PIR; S29675; S29675.
DR HSSP; P56252; IPDY.
DR SWISS-2DPAGE; P21550; MOUSE.

DR MGD; MGI:95395; Eno3.
DR InterPro: IPR000941; Enolase.
DR Pfam: PF00113; enolase; 1.
DR PRINTS: PR00148; ENOLASE.
DR ProDom: PD000902; Enolase; 1.
DR PROSITE: PS00164; ENOLASE; 1.
KW Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT_MET 0
FT ACT_SITE 157 157
FT METAL 244 244
FT METAL 292 292
FT METAL 317 317
FT CONFLICT 233 234
SO SEQUENCE 433 AA; 46893 MW; B318B763382D3FA8 CRC64;
BY SIMILARITY.
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
AG -> NA (IN REF. 3).
Query Match
Best Local Similarity 72.2%; Score 65; DB 1; Length 433;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
OY 1 LVVGLCTGQIKTGAPC 16
DB 383 LVVGLCTGQIKTGAPC 398

RESULT 12
ENOB_RABBIT
ID ENOB_RABBIT STANDARD: PRT: 433 AA.
AC P25704; Q9N0N6;
DT 01-MAY-1992 (Rel. 22, Created)
DT 20-AUG-2001 (Rel. 40, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
GN ENO3.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE.
RX MEDLINE=9113295; PubMed=2275753;
RA Chin C.C.O.;
RT "The primary structure of rabbit muscle enolase.";
RL J. Protein Chem. 9:427-432(1990).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Muscle;
RA Zheng S.-X.;
RT "The cDNA cloning of rabbit muscle-specific enolase gene, site
directed mutagenesis (P417L) of the gene, expression of the wild-type
and mutant genes in Escherichia coli.";
RLthesis (1995), Concordia University, Montreal / Quebec, Canada.
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
+ H(2)O.
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC -----
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CC -----

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CC -----
CC EMBL: AF260259; AAF71925.1; -.
CC PIR: A37210; A37210.
CC HSP: P56252; 1PDX.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lysase: Glycolysis; Magnesium family.
CC INT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC CONFLICT 253 253 N -> D (IN REF. 1).
CC CONFLICT 296 296 N -> D (IN REF. 1).
CC SEQUENCE 433 AA; 46859 MM; 063A4005443C0403 CRC64;

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Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

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RESULT 13
ENOB_RAT STANDARD; PRT; 433 AA.
AC P15429;
DT 01-APR-1990 (Rel. 14, Created)
DT 01-APR-1990 (Rel. 14, Last sequence update)
DT 15-JUL-1998 (Rel. 36, Last annotation update)
DE BETA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (SKELETAL MUSCLE ENOLASE).
DE ENO3 OR ENO-3.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
OX [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Wistar;
RC MEDLINE=8912113; PubMed=2914621;
RA Ohshima Y., Mitsui H., Takayama Y., Kushiya E., Sakimura K.,
RA Takahashi Y.;
RA "cDNA cloning and nucleotide sequence of rat muscle-specific enolase
(beta beta enolase).";
RT FEBS Lett. 242:425-430(1989).
RN [2]
RP SEQUENCE OF 1-27 FROM N.A.
RX MEDLINE=91099531; PubMed=2269373;
RA Sakimura K., Kushiya E., Ohshima-Ichikawa Y., Mitsui H.,
RA Takahashi Y.;
RA "Structure and expression of rat muscle-specific enolase gene.";
RT FEBS Lett. 277:78-82(1990)
RL
CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
CC + H(2O).
CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
CC THE DIMER.
CC -1- PATHWAY: GLYCOLYSIS.
CC -1- SUBUNIT: HOMODIMER.
CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
CC FOUND ONLY IN NERVOUS TISSUE.
CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
CC This Swiss-Prot entry is copyright. It is produced through a collaboration

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CC or send an email to license@isb-sib.ch).
CC -----

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CC EMBL: Y00979; CA68788.1; -.
CC PIR: S02072; S02072.
CC HSP: P56252; 1PDX.
CC InterPro: IPR000941; Enolase.
CC Pfam: PF00113; enolase; 1.
CC PRINTS: PR00148; ENOLASE.
CC ProDom: PD000902; ENOLASE; 1.
CC PROSITE: PS00164; ENOLASE; 1.
CC Lysase: Glycolysis; Magnesium family.
CC INT_MET 0
CC ACT_SITE 157 157 BY SIMILARITY.
CC METAL 244 244 MAGNESIUM (BY SIMILARITY).
CC METAL 292 292 MAGNESIUM (BY SIMILARITY).
CC METAL 317 317 MAGNESIUM (BY SIMILARITY).
CC SEQUENCE 433 AA; 46829 MM; 4C2CDB12DBA536D CRC64;

```

```

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 LVVGLCTGQIKTGAPC 16
Db 383 LVVGLCTGQIKTGAPC 398

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RESULT 14
ENOB_HUMAN STANDARD; PRT; 433 AA.
AC P09104;
DT 01-MAR-1989 (Rel. 10, Created)
DT 01-MAR-1989 (Rel. 10, Last sequence update)
DT 20-AUG-2001 (Rel. 40, Last annotation update)
DE GAMMA ENOLASE (EC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
DE (NEURAL ENOLASE) (NSE).
DE ENO2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
OX [1]
RP SEQUENCE FROM N.A. AND PARTIAL SEQUENCE.
RC TISSUE=Retina;
RC MEDLINE=89091176; PubMed=3208766;
RA McAlreese S.M., Dunbar B., Forthright J., Hinks L., Day I.N.M.;
RT "Complete amino acid sequence of the neurone-specific gamma isozyme
of enolase (NSE) from human brain and comparison with the
non-neuronal alpha form (NNE).";
RT Eur. J. Biochem. 178:413-417(1988).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=9006764; PubMed=2792767;
RA Oliva D., Barba G., Barbieri G., Giallongo A., Feo S.;
RA "Cloning, expression and sequence homologies of cDNA for human gamma
enolase.";
RL Gene 79:355-360(1989).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain;
RX MEDLINE=88259288; PubMed=3385803;
RA van Obberghen E., Kamholz J., Bishop J.G. III, Zomzely-Neurath C.,
RA Lazzarini R.A.;
RT "Human gamma enolase: isolation of a cDNA clone and expression in
normal and tumor tissues of human origin.";
RL J. Neurosci. Res. 19:450-456(1988).

```

[4]
 RN SEQUENCE FROM N.A.
 RP TISSUE-Hematopoietic;
 RX MEDLINE=91257823; PubMed=2045099;
 RT Oliva D., Call L., Rao S., Giallongo A.;
 RT "Complete structure of the human gene encoding neuron-specific
 RT enolase.";
 RL Genomics 10:157-165(1991).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=96303695; PubMed=8723724;
 RA Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E.,
 RA Spanos S., Malley T., Gibbs R.A.;
 RT "A gene-rich cluster between the CD4 and triosephosphate isomerase
 RT genes at human chromosome 12p13.";
 RL Genome Res. 6:314-326(1996).
 RN [6]
 RP SEQUENCE OF 424-433 FROM N.A.
 RX MEDLINE=88005129; PubMed=3653393;
 RA Day I.N.M., Allsopp M.T.E.P., Moore D.C.M., Thompson R.J.;
 RT "Sequence conservation in the 3'-untranslated regions of neurone-
 RT specific enolase, lymphokine and protooncogene mRNAs.";
 RL FEBS Lett. 222:139-143(1987).
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
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 CC -----
 DR EMBL: X13120; CAA31512.1; -
 DR EMBL: M22349; AAB59554.1; -
 DR EMBL: M36768; AAB52388.1; ALT_INIT.
 DR EMBL: X51956; CAA36215.1; -
 DR EMBL: U47924; AAB51320.1; -
 DR EMBL: X14327; CAA32505.1; -
 DR PIR: J00060; NOHUG.
 DR PIR: S02077; S02077.
 DR PIR: S02616; S02616.
 DR HSSP: P56252; 1PDY.
 DR MIM: 131360; -
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.
 KW Lyase; Glycolysis; Magnesium; Multigene family; Polymorphism.
 FT INIT_MET 0
 FT ACET_SITE 157 157
 FT METAL 244 244
 FT METAL 292 292
 FT METAL 317 317
 FT VARIANT 263 263
 FT VARIANT 394 394
 FT VARIANT 394 394
 FT CONFLICT 3 3
 FT CONFLICT 26 27
 FT CONFLICT 126 126
 E -> N (IN REF. 3).
 E -> N (IN REF. 3).

FT CONFLICT 239 239 M -> I (IN REF. 2, 3, 4 AND 5).
 SQ SEQUENCE 433 AA; 47154 MW; 0F01A8A5FF9152A1 CRC64;
 Query Match 72.2%; Score 65; DB 1; Length 433;
 Best Local Similarity 81.2%; Pred. No. 0.0043;
 Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;
 QY 1 LVVGLCTQCIKTPAC 16
 Db 383 LVVGLCTQCIKTPAC 398
 RESULT 15
 ENOG_MOUSE
 ID ENOG_MOUSE STANDARD; PRT; 433 AA.
 AC P17183;
 DT 01-AUG-1990 (Rel. 15, Created)
 DT 01-AUG-1990 (Rel. 15, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE GAMMA ENOLASE (RC 4.2.1.11) (2-PHOSPHO-D-GLYCERATE HYDRO-LYASE)
 DE (NEURAL ENOLASE) (NSE).
 GN ENO2 OR ENO-2.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-Brain;
 RX MEDLINE=90301487; PubMed=2362815;
 RA Raghad M., Dumont X., Chalton P., Lelias J.M., Lamande N., Lucas M.,
 RA Lazar M., Caput D.;
 RT "Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from
 RT mouse brain.";
 RL Nucleic Acids Res. 18:3638-3638(1990).
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ansari-Lari M.A., Oeltjen J.C., Schwartz S., Zhang Z., Muzny D.M.,
 RA Lu J., Gorrell J.H., Chinnait A.C., Belmont J.W., Miller W.,
 RA Gibbs R.A.;
 RL Submitted (AUG-1997) to the EMBL/GenBank/DBJ databases.
 CC -1- CATALYTIC ACTIVITY: 2-PHOSPHO-D-GLYCERATE = PHOSPHOENOLPYRUVATE
 CC + H(2)O.
 CC -1- COFACTOR: MAGNESIUM IS REQUIRED FOR CATALYSIS AND FOR STABILIZING
 CC THE DIMER.
 CC -1- PATHWAY: GLYCOLYSIS.
 CC -1- SUBUNIT: HOMODIMER.
 CC -1- SUBCELLULAR LOCATION: CYTOPLASMIC.
 CC -1- TISSUE SPECIFICITY: THREE CLASSES OF ENOLASE ISOENZYMES HAVE BEEN
 CC IDENTIFIED IN MAMMALIAN TISSUES. ISOENZYME ALPHA IS PRESENT IN
 CC MOST TISSUES, BETA IS LOCALIZED IN MUSCLE TISSUE, AND GAMMA IS
 CC FOUND ONLY IN NERVOUS TISSUE.
 CC -1- SIMILARITY: BELONGS TO THE ENOLASE FAMILY.
 CC -----
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 CC -----
 DR EMBL: X52380; CAA36606.1; -
 DR EMBL: AC002397; AAC36002.1; -
 DR PIR: S10247; S10247.
 DR HSSP: P56252; 1PDY.
 DR MGD: MGI:95394; Eno2.
 DR InterPro: IPR000941; Enolase.
 DR Pfam: PF00113; enolase; 1.
 DR PRINTS: PR00148; ENOLASE.
 DR ProDom: PD000902; Enolase; 1.
 DR PROSITE: PS00164; ENOLASE; 1.

KM Lyase; Glycolysis; Magnesium; Multigene family.
FT INIT_MER 0 157
FT ACT_SITE 157 157
FT METAL 244 244
FT METAL 292 292
FT METAL 317 317
SQ SEQUENCE 433 AA; 47165 MW; B7281132E637D43E CRC64;

Query Match 72.2%; Score 65; DB 1; Length 433;
Best Local Similarity 81.2%; Pred. No. 0.0043;
Matches 13; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 LVVGLCTCQIKTGAPC 16
|||||
DB 383 LVVGLCTGQIKTGAPC 398

Search completed: May 8, 2002, 11:46:32
Job time: 108 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:45:50 ; Search time 12.85 Seconds
(without alignments)
94.848 Million cell updates/sec

Title: US-09-647-457-2

Perfect score: 16
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 219241 seqs, 76174552 residues

Word size : 0

Total number of hits satisfying chosen parameters: 219241

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	7	43.8	335	2 A39579	c-myc promoter-bin
2	7	43.8	395	2 I50026	phosphopyruvate hy
3	7	43.8	433	2 A23850	phosphopyruvate hy
4	7	43.8	433	2 A37210	phosphopyruvate hy
5	7	43.8	434	1 NOHUG	phosphopyruvate hy
6	7	43.8	434	1 NOMSB	phosphopyruvate hy
7	7	43.8	434	1 NOXL	phosphopyruvate hy
8	7	43.8	434	2 A24742	phosphopyruvate hy
9	7	43.8	434	2 S10246	phosphopyruvate hy
10	7	43.8	434	2 S10247	phosphopyruvate hy
11	7	43.8	434	2 A29170	phosphopyruvate hy
12	7	43.8	434	2 A32132	phosphopyruvate hy
13	7	43.8	434	2 S02072	phosphopyruvate hy
14	7	43.8	434	2 S06756	phosphopyruvate hy
15	7	43.8	434	2 UC4186	phosphopyruvate hy
16	7	43.8	434	2 UC4187	phosphopyruvate hy
17	7	43.8	434	2 JC1039	phosphopyruvate hy
18	7	43.8	434	2 A23126	phosphopyruvate hy
19	7	43.8	458	2 I37360	phosphopyruvate hy
20	6	37.5	142	2 S04071	hemoglobin alpha c
21	6	37.5	231	2 D64486	hypothetical prote
22	6	37.5	517	2 D86264	protein F3f19.6 (1
23	6	37.5	727	2 T10616	hypothetical prote
24	5	31.2	34	2 C43853	phosphopyruvate hy
25	5	31.2	72	2 T00181	hypothetical prote
26	5	31.2	73	2 T30612	hypothetical prote
27	5	31.2	85	2 H69191	hypothetical prote
28	5	31.2	88	2 C64697	flagellar biosynth
29	5	31.2	88	2 C82472	conserved hypothet

30	5	31.2	91	2 T45346	hypothetical prote
31	5	31.2	94	1 JC4508	flagellar biosynth
32	5	31.2	97	1 FEPR	ferredoxin [2Fe-2S
33	5	31.2	99	2 T40428	60S ribosomal prot
34	5	31.2	99	2 T43238	ribosomal protein
35	5	31.2	106	2 T45612	ferredoxin [2Fe-2S
36	5	31.2	110	2 C24775	T-cell receptor ga
37	5	31.2	111	2 G83480	cytochrome c ubiq
38	5	31.2	111	2 T09899	hypothetical prote
39	5	31.2	116	2 B75550	hypothetical prote
40	5	31.2	118	2 C84859	hypothetical prote
41	5	31.2	120	1 DER2N3	NADH dehydrogenase
42	5	31.2	120	2 S27251	NADH dehydrogenase
43	5	31.2	120	2 S58557	NADH dehydrogenase
44	5	31.2	121	2 T09824	plantacyanin precu
45	5	31.2	121	2 D84128	hypothetical prote

ALIGNMENTS

RESULT 1

A39579 c-myc promoter-binding protein MBP-1 - human

C:Species: Homo sapiens (man)

C:Date: 07-Feb-1992 #sequence revision 07-Feb-1992 #text_change 22-Jun-1999

C:Accession: A39579

R:Ray, R.; Miller, D.M.

Mol. Cell. Biol. 11, 2154-2161, 1991

A:Title: Cloning and characterization of a human c-myc promoter-binding protein.

A:Reference number: A39579; MUID:91172204

A:Accession: A39579

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-335 <RAY>

A:Cross-references: GB:M55914; NID:g180662; PIDN:AAA35698.1; PID:g180663

A:Genetics:

A:Gene: GDB:MBP1

A:Cross-references: GDB:127383

A:Map position: 8p11.2-8p11.1

C:Superfamily: enolase

C:Keywords: DNA binding; nucleus; transcription regulation

Query Match 43.8%; Score 7; DB 2; Length 335;

Best Local Similarity 100.0%; Pred.No. 2.6;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
|||||
Db 285 LVVGLCT 291

RESULT 2

I50026 phosphopyruvate hydratase (EC 4.2.1.11) alpha - American alligator (fragment)

N:Alternate names: alpha-enolase

C:Species: Alligator mississippiensis (American alligator)

C:Date: 21-Feb-1997 #sequence revision 21-Feb-1997 #text_change 22-Jun-1999

C:Accession: I50026

R:Adges, S.B.

Proc. Natl. Acad. Sci. U.S.A. 91, 2621-2624, 1994

A:Title: Molecular evidence for the origin of birds.

A:Reference number: A53470; MUID:94195794

A:Accession: I50026

A:Status: preliminary; nucleic acid sequence not shown; translation not shown; tra

A:Molecule type: mRNA

A:Residues: 1-395 <HBD>

A:Cross-references: GB:L28078; NID:g472796; PIDN:AAA53671.1; PID:g472797

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; hydro-lyase

Query Match 43.8%; Score 7; DB 2; Length 395;
Best Local Similarity 100.0%; Pred. No. 3;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
|||||||
DB 362 LVVGLCT 368

RESULT 3
A23850
phosphopyruvate hydratase (EC 4.2.1.11), skeletal muscle - chicken
N:Alternate names: enolase, skeletal muscle
C:Species: Gallus gallus (chicken)
C>Date: 22-Jul-1987 #sequence revision 22-Jul-1987 #text_change 17-Mar-1999
A:Accession: A23850; A60809
R:Russell, G.A.; Dunbar, B.; Fothergill-Gilmore, L.A.
Biochem. J. 236, 115-126, 1986
A:Title: The complete amino acid sequence of chicken skeletal-muscle enolase.
A:Reference number: A23850; MUID:87075592
A:Accession: A23850
A:Molecule type: protein
A:Residues: 1-433 <RUS>
R:Gibson, B.W.; Daley, D.J.; Williams, D.H.
Anal. Biochem. 169, 217-226, 1988
A:Title: Structural elucidation of N-terminal post-translational modifications by mass spectrometry

A:Reference number: A60809; MUID:88250539
A:Accession: A60809
A:Molecule type: protein
A:Residues: 1-9 <GIB>
C:Comment: Several tissue-specific enolase isoenzymes are found in vertebrates.
C:Superfamily: enolase
C:Keywords: acetylated amino end; carbon-oxygen lyase; gluconeogenesis; glycolysis; hydrolysis; modified site: acetylated amino end (Ser) #status experimental
F:19/Binding site: magnesium 2 (Ser) #status predicted
F:209/Active site: Glu #status predicted
F:244,292,311/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match 43.8%; Score 7; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
|||||||
DB 383 LVVGLCT 389

RESULT 4
A37210
phosphopyruvate hydratase (EC 4.2.1.11) beta - rabbit
N:Alternate names: enolase beta
C:Species: Oryctolagus cuniculus (domestic rabbit)
C>Date: 30-Dec-1991 #sequence revision 30-Dec-1991 #text_change 05-Aug-1994
A:Accession: A37210
R:Chin, C.C.C.
J. Protein Chem. 9, 427-432, 1990
A:Title: The primary structure of rabbit muscle enolase.
A:Reference number: A37210; MUID:91113295
A:Accession: A37210
A:Molecule type: preliminary
A:Residues: 1-433 <CHI>
C:Superfamily: enolase
C:Keywords: acetylated amino end; carbon-oxygen lyase; hydro-lyase
F:1/Modified site: acetylated amino end (Ala) #status experimental

Query Match 43.8%; Score 7; DB 2; Length 433;
Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGLCT 7
|||||||
DB 383 LVVGLCT 389

RESULT 5
NOHUG
phosphopyruvate hydratase (EC 4.2.1.11) gamma - human
N:Alternate names: enolase gamma; neuron-specific enolase
C:Species: Homo sapiens (man)
C>Date: 31-Mar-1990 #sequence revision 31-Mar-1990 #text_change 18-Jun-1999
A:Accession: J00060; S16163; S02077; I56569; S02616; S38303
R:Oliva, D.; Barba, G.; Barbieri, G.; Giallongo, A.; Feo, S.
Gene 79, 355-360, 1989
A:Title: Cloning, expression and sequence homologies of cDNA for human gamma enolase.
A:Reference number: J00060; MUID:90006764
A:Accession: J00060
A:Molecule type: mRNA
A:Residues: 1-434 <OLA>
A:Cross-references: GB:M22349; NID:9951199; PIDN:AA59554.1; PID:9182116; GB:M27833
R:Oliva, D.; Gall, L.; Feo, S.; Giallongo, A.
Genomics 10, 157-165, 1991
A:Title: Complete structure of the human gene encoding neuron-specific enolase.
A:Reference number: S16163; MUID:91257823
A:Accession: S16163
A:Molecule type: DNA
A:Residues: 1-434 <OLA>
A:Cross-references: GB:X51956; NID:931164; PIDN:CAA36215.1; PID:931165
R:McLeese, S.M.; Dunbar, B.; Fothergill, J.E.; Hinks, L.J.; Day, I.N.M.
Eur. J. Biochem. 178, 413-417, 1988
A:Title: Complete amino acid sequence of the neuron-specific gamma isozyme of enolase.
A:Reference number: S02077; MUID:89091176
A:Accession: S02077
A:Molecule type: mRNA
A:Residues: 2-3, 'O', '5'-239, 'M', '241-434 <MCAS>
A:Cross-references: EMBL:X13120; NID:931145; PIDN:CAA31512.1; PID:9930063
A:Note: part of this sequence was confirmed by protein sequencing
A:Note: 264-Ala and 395-Ala were also found
R:Van Obergerghen, L.; Kamholz, J.; Bishop, J.G.
J. Neurosci. Res. 19, 450-456, 1988
A:Title: Human gamma enolase: isolation of a cDNA clone and expression in normal and tumor cells
A:Reference number: I56569; MUID:88259288
A:Accession: I56569
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 'GC', '29-126', 'N', '128-434 <VAN>
A:Cross-references: GB:M26768; NID:9182117; PIDN:AA52388.1; PID:9182118
R:Day, I.N.M.; Allsopp, M.T.E.P.; Moore, D.C.M.; Thompson, R.J.
FEBS Lett. 222, 139-143, 1987
A:Title: Sequence conservation in the 3'-untranslated regions of neuron-specific enolase
A:Reference number: S02616; MUID:88005129
A:Accession: S02616
A:Status: not compared with conceptual translation
A:Molecule type: mRNA
A:Residues: 425-434 <DAY>
A:Cross-references: GB:J00061; GB:M27833
R:Harrington, C.R.; Quinn, G.B.; Hurt, J.; Day, I.N.M.; Wischik, C.M.
Biochim. Biophys. Acta 1158, 120-128, 1993
A:Title: Characterisation of an epitope specific to the neuron-specific isoform of enolase
A:Reference number: S38303; MUID:94002176
A:Accession: S38303
A:Molecule type: protein
A:Residues: 156-173 <HAR>
C:Comment: Enolase occurs with at least three isoforms (alpha, beta, and gamma) in mammals. The Thr-191 may be important for the enhanced tolerance to chloride ions of the gamma isoform.
C:Genetics:
A:Gene: GDB:ENO2
A:Cross-references: GDB:119872; OMIM:131360
A:Map position: 12p13-12p13
A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/2; 412/2
C:Complex: homodimer
C:Function:

A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to phosphoenolpyruvate
A:Pathway: gluconeogenesis; glycolysis
C:Superfamily: enolase
C:Keywords: blocked amino end; brain; carbon-oxygen lyase; gluconeogenesis; glycolysis;
P-2-334/product: phosphopyruvate hydratase gamma #status predicted <MAN>
F-2/Modified site: blocked amino end (Ser) (in mature form) #statit# acetylated
F-40/Binding site: magnesium 2 (Ser) #status predicted
F-210/345/Active site: Glu, Lys #status predicted
F-7245,293,318/Binding site: magnesium 1 (Asp,Glu, Asp) #status predicted

Query Match	43.8%	Score 7	DB 1	Length 434
Best Local Similarity	100.0%	Pred. No. 3.2		
Matches 7, Conservative	0	Mismatches 0	Indels 0	Gaps 0

QY	1	L V G L C T	7
Db	384	L V G L C T	390

RESULT	6
NOMSB	

phosphohypruvinate hydratase (EC 4.2.1.11) beta - mouse
N.Alternate names: enolase beta
C.Species: Mus musculus (house mouse)
C.Date: 31-Mar-1992 #sequence_revision 31-Mar-1992 #text_change 18-Jun-1999
C.Accession: S17109, S18036, S29675, A33921
R.Liemande, N.; Brosset, S.; Keller, A.; Lucas, M.; Lazar, M.
submitted to the EMBL Data Library, September 1991
A.Reference number: S17109
A.Accession: S17109
A.Molecule type: DNA
A.Residues: 1-434 <LA2>
A.Cross-references: EMBL:X61600; NID:g50848; PIDN:CAA43797.1; PID:g50849
R.Peterson, C.A.; Cho, M.; Rastinejad, F.; Blau, H.M.
submitted to the EMBL Data Library, October 1991
A.Description: Beta-enolase: a gene expressed in undifferentiated postnatal myoblasts th
A.Reference number: S18036
A.Accession: S18036
A.Molecule type: mRNA
A.Residues: 1-434 <PET>
A.Cross-references: EMBL:X62667; NID:g50143; PIDN:CAA4540.1; PID:g50144
R.Lazar, M.; Liemande, N.; Brosset, S.; Lucas, M.; Keller, A.
submitted to the EMBL Data Library, February 1991
A.Reference number: S29675
A.Accession: S29675
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 1-434 <LA2>
A.Cross-references: EMBL:X57247; NID:g50846; PIDN:CAA40913.1; PID:g50847
R.Liemande, N.; Mazo, A.M.; Lucas, M.; Montarras, D.; Pinsel, C.; Gros, F.; Legault-Demard
Proc. Natl. Acad. Sci. U.S.A. 86, 4445-4449, 1989
A.Title: Murine muscle-specific enolase-cDNA cloning, sequence, and developmental expre
A.Reference number: A33921, NMID:89282789
A.Accession: A33921
A.Status: preliminary
A.Molecule type: mRNA
A.Residues: 59-233, 'NA', 236-434 <LA2>
A.Cross-references: GB:M20745; NID:g193029; PIDN:AAA37554.1; PID:g387144
A.Experimental source: skeletal muscle
C.Genetics: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
A.Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2
C.Function:
A.Description: catalyzes the reversible dehydration of 2-phospho-D-glycetric acid to phosph
A.Pathway: gluconeogenesis; glycolysis
C.Superfamily: enolase
C.Keywords: carbon-carbon lyase; carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis
F:40/Binding site: magnesium 2 (Ser) #status predicted
F:210,343/Active site: Glu, Lys #status predicted
F:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Best Local Similarity 100.0%; Pred. No. 3.2;
Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	LVGGLCT	7
Db	384	LVGGLCT	390

RESULT	7
NOXL	

phosphopyruvate hydratase (EC 4.2.1.11) ENO1 - African clawed frog
 N:Alternative names: enolase ENO1
 C:Species: Xenopus laevis (African clawed frog)
 C:Date: 31-Mar-1991 #sequence_revision 31-Mar-1991 #text_change 18-Jun-1999
 C:Accession: S00463
 R:Segall, N.; Shukrowski, A.; Dworkin, M.B.; Dworkin-Rastl, E.
 Biochem. J. 251, 31-39, 1988
 A:Title: Enolase isoenzymes in adult and developing *Xenopus laevis* and characterization
 A:Reference number: S00463; MUID:88268812
 A:Accession: S00463
 A:Molecule type: mRNA
 A:Residues: 1-434 <SEG>
 A:Cross-references: EMBL:Y00718; NID:g64679; PIDN:CA68706.1; PID:g64680
 C:Genetics:
 A:Gene: ENO1
 C:Function:
 A:Description: catalyzes the reversible dehydration of 2-phospho-D-glyceric acid to
 A:Pathway: gluconeogenesis; glycolysis
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; dimer; gluconeogenesis; glycolysis; hydro-lyase; r
 E:40/Binding site: magnesium 2 (ser) #status predicted
 E:210,343/Active site: Glu, Lys #status predicted
 E:245,293,318/Binding site: magnesium 1 (Asp, Glu, Asp) #status predicted

Query Match	43.8%	Score 7:	DB 1:	Length 434:
Best Local Similarity	100.0%	Pred. No. 3.2:		
Matches 7: Conservative	0:	Mismatches	0:	Indels 0:
				Gaps 0:

QY	1	L	V	G	L	C	T	7
		1	1	1	1	1	1	
Db	384	L	V	G	L	C	T	390

RESULT 8
A24742

N:phosphogluvurate hydratase (EC 4.2.1.11) gamma - rat
 A:Alternate names: 2-phospho-glycerate dehydratase; enolase gamma; neuronal enolase
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 25-Oct-1987 #sequence revision 25-Oct-1987 #text-change 22-Jun-1999
 C:Accession: A24742; PQ0006
 R:Sakimura, K.; Kushiya, E.; Obinata, M.; Odani, S.; Takahashi, Y.
 Proc. Natl. Acad. Sci. U.S.A. 82, 7453-7457, 1985
 A:Title: Molecular cloning and the nucleotide sequence of cDNA for neuron-specific
 A:Reference number: A24742; MUID:86042683
 A:Accession: A24742
 A:Molecule type: mRNA
 A:Residues: 1-434 <SAK>
 A:Cross-references: GB:M11931; NID:g204041; PIDN:AAA41119.1; PID:g204042
 R:Sakimura, K.; Kushiya, E.; Takahashi, Y.; Suzuki, Y.
 Gene 60, 103-113, 1987
 A:Title: The structure and expression of neuron-specific enolase gene.
 A:Reference number: PQ0006; MUID:88152493
 A:Accession: PQ0006
 A:Molecule type: DNA
 A:Residues: 1-28 <SA2>
 A:Cross-references: GB:M22770; GB:M18742; NID:g205766; PIDN:AAA41725.1; PID:g554480
 C:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
|||||
Db 384 LVVGICT 390

RESULT 9

S10246

phosphopyruvate hydratase (EC 4.2.1.11) alpha - mouse

N:Alternate names: 2-phosphoglycerate dehydratase; enolase alpha

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence-revision 12-Feb-1993 #text-change 22-Jun-1999

C:Accession: S10246; A56781

R:Kaghad, M.; Dumont, X.; Chalou, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res. 18, 3638, 1990

A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.

A:Reference number: S10246; MUID:90301487

A:Accession: S10246

A:Molecule type: mRNA

A:Residues: 1-434 <KAG>

A:Cross-references: EMBL:X53328; NID:955490; PIDN:CAA36605.1; PID:955491

R:Bottillo, L.A.; Kendrick, N.C.; Keller, A.; Li, Y.; Tabas, I.

Arterioscler. Thromb. 13, 264-275, 1993

A:Title: Cholesteryl ester loading of mouse peritoneal macrophages is associated with ch

sterol

A:Reference number: A56781; MUID:93152553

A:Accession: A56781

A:Status: preliminary

A:Molecule type: protein

A:Residues: 'X', 60, 'X', 62-67, 'X', 69-71, 'XX', 100-109, 'X', 111-112, 'X', 114, 'X', 184-185, 'X',

A:Experimental source: peritoneal macrophages

A:Note: sequence modified after extraction from NCBI backbone

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

QY 1 LVVGICT 7
|||||

Db 384 LVVGICT 390

RESULT 10

S10247

phosphopyruvate hydratase (EC 4.2.1.11) gamma - mouse

N:Alternate names: 2-phosphoglycerate dehydratase; enolase gamma

C:Species: Mus musculus (house mouse)

C:Date: 12-Feb-1993 #sequence-revision 12-Feb-1993 #text-change 22-Jun-1999

C:Accession: S10247

R:Kaghad, M.; Dumont, X.; Chalou, P.; Lelias, J.M.; Lamande, N.; Lucas, M.; Lazar, M.; C

Nucleic Acids Res. 18, 3638-1990

A:Title: Nucleotide sequences of cDNAs alpha and gamma enolase mRNAs from mouse brain.

A:Reference number: S10246; MUID:90301487

A:Accession: S10247

A:Molecule type: mRNA

A:Residues: 1-434 <RAG>

A:Cross-references: EMBL:X52380; NID:955494; PIDN:CAA36606.1; PID:955495

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 43.8%; Score 7; DB 2; Length 434;

Best Local Similarity 100.0%; Pred. No. 3.2;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVVGICT 7
|||||
Db 384 LVVGICT 390

RESULT 11

A29170

phosphopyruvate hydratase (EC 4.2.1.11) alpha - human

N:Alternate names: 2-phosphoglycerate dehydratase; enolase 1; enolase alpha

C:Species: Homo sapiens (man)

C:Date: 19-Nov-1988 #sequence-revision 19-Nov-1988 #text-change 20-Jun-2000

C:Accession: S11696; A29170; S52858; A39183

R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Showe, L.C.

Eur. J. Biochem. 190, 567-573, 1990

A:Title: Structure of the human gene for alpha-enolase.

A:Reference number: S11696; MUID:90323004

A:Accession: S11696

A:Molecule type: DNA

A:Residues: 1-434 <GTA>

A:Cross-references: EMBL:X16288; NID:931172; PIDN:CAA4360.1; PID:91167843

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, August 1989

R:Giallongo, A.; Feo, S.; Moore, R.; Croce, C.M.; Showe, L.C.

Proc. Natl. Acad. Sci. U.S.A. 83, 6741-6745, 1986

A:Title: Molecular cloning and nucleotide sequence of a full-length cDNA for human

A:Reference number: A29170; MUID:86313654

A:Accession: A29170

A:Molecule type: mRNA

A:Residues: 1-434 <GTA>

A:Cross-references: GB:M4328; NID:9182113; PIDN:AAA52387.1; PID:9182114

A:Note: the authors translated the codon AAG for residue 193 as His

R:Walter, M.; Leidenberger, F.A.; Schweppe, K.W.; Berg, H.; Northmann, W.

submitted to the EMBL Data Library, February 1995

A:Description: Autoreactive epitopes within the human alpha-enolase and their recog

A:Reference number: S52858

A:Accession: S52858

A:Molecule type: protein

A:Residues: 1-251, 'S', 253-434 <NAL>

A:Cross-references: EMBL:X84907; NID:9693932; PIDN:CAA59331.1; PID:9693933

A:Experimental source: endometrium carcinoma cell line HEC-1B

R:Miles, L.A.; Dahlberg, C.M.; Plescia, J.; Felez, J.; Kato, K.; Plov, E.F.

Biochemistry 30, 1682-1691, 1991

A:Title: Role of cell-surface lysines in plasminogen binding to cells: identification

A:Reference number: A39183; MUID:91129243

A:Accession: A39183

A:Molecule type: protein

A:Residues: 170-182, 'I', 184, 'R', 186-190, 245-252 <MIL>

A:Gene: GDB: ENO1

A:Cross-references: GDB:119871; OMIM:172430

A:Map position: 1p36-1p36

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2

C:Function:

A:Description: catalyzes the reversible hydration of phosphoenolpyruvate to 2-phosp

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; magnesiu

F.2-434/Product: phosphopyruvate hydratase alpha #status predicted <MAY>

QY 1 LVVGICT 7
|||||

Db 384 LVVGICT 390

RESULT 12

A52132

phosphopyruvate hydratase (EC 4.2.1.11) alpha - duck

N:Alternate names: enolase alpha; tau-crystallin

C:Species: Anas platyrhynchos (domestic duck)

C:Date: 21-May-1990 #sequence-revision 21-May-1990 #text-change 21-Jul-2000

C:Accession: A52132

R:Wistow, G.J.; Lietman, T.; Williams, L.A.; Stapel, S.O.; de Jong, W.W.; Horwitz,

J. Cell Biol. 107, 2729-2736, 1988
 A:Title: Tau-crystallin/alpha-enolase: one gene encodes both an enzyme and a lens struct
 A:Reference number: A92750; MUID:89079778
 A:Accession: A32132
 A:Molecule type: mRNA
 A:Residues: 1-434 <WIS>
 A:Cross-references: GB:X14195; NID:962455; PIDN:CAA32409.1; PID:962456
 A:Superfamily: enolase
 C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

RESULT 13

S02072
 phosphopyruvate hydratase (EC 4.2.1.11) beta - rat
 N:Alternate names: enolase beta; enolase, muscle-specific
 C:Species: Rattus norvegicus (Norway rat)
 C:Date: 01-Dec-1989 #sequence_revision 01-Dec-1989 #text_change 22-Jun-1999
 C:Accession: S02072

R:Ohshima, Y.; Mitsui, H.; Takayama, Y.; Kushiya, E.; Sakimura, K.; Takahashi, Y.
 FEBS Lett. 242, 425-430, 1989

A:Title: cDNA cloning and nucleotide sequence of rat muscle-specific enolase (beta-beta
 A:Reference number: S02072; MUID:89121113
 A:Accession: S02072

A:Molecule type: mRNA

A:Residues: 1-434 <OHS>

A:Cross-references: EMBL:X00979; NID:957781; PIDN:CAA68788.1; PID:957782

A:Note: the sequence from Fig. 4 is inconsistent with that from Fig. 2 in having 40-Asp

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

RESULT 14

S06756
 phosphopyruvate hydratase (EC 4.2.1.11) beta - human

N:Alternate names: enolase beta; enolase, skeletal muscle; phosphopyruvate hydratase, m

C:Species: Homo sapiens (man)

C:Date: 22-Jan-1993 #sequence_revision 22-Jan-1993 #text_change 22-Jun-1999

C:Accession: S06756; S14759; S15933; S33330; S08685; S31650

R:Peshavaria, M.; Hinks, L.J.; Day, I.N.M.

Nucleic Acids Res. 17, 8862, 1989

A:Title: Structure of human muscle (beta) enolase mRNA and protein, deduced from a genom

A:Reference number: S06756; MUID:90067857

A:Accession: S06756

A:Molecule type: mRNA

A:Residues: 1-434 <PES>

A:Cross-references: EMBL:X16504; NID:931169; PIDN:CAA34513.1; PID:931170

R:Peshavaria, M.; Day, I.N.M.

Biochem. J. 275, 427-433, 1991

A:Title: Molecular structure of the human muscle-specific enolase gene (ENOS3).

A:Reference number: S14759; MUID:91222137

A:Accession: S14759

A:Status: nucleic acid sequence not shown

A:Molecule type: DNA

A:Residues: 1-434 <PE2>

A:Cross-references: EMBL:X55976

R:Call, L.; Feo, S.; Oliva, D.; Giallongo, A.
 Nucleic Acids Res. 18, 1893, 1990

A:Title: Nucleotide sequence of a cDNA encoding the human muscle-specific enolase

A:Reference number: S15933; MUID:90245587

A:Accession: S15933

A:Molecule type: mRNA

A:Residues: 1-84, 'A', 86-161, 'K', 163-434 <CAL>

A:Cross-references: EMBL:X51957; NID:934788; PIDN:CAA36216.1; PID:934789

R:Giallongo, A.; Venturella, S.; Oliva, D.; Barbieri, G.; Rubino, P.; Feo, S.

Eur. J. Biochem. 214, 367-374, 1993

A:Title: Structural features of the human gene for muscle-specific enolase. Differ

A:Reference number: S33330; MUID:93292497

A:Accession: S33330

A:Status: nucleic acid sequence not shown; translation not shown

A:Molecule type: DNA

A:Residues: 1-161, 'K', 163-434 <GIN>

A:Cross-references: EMBL:X56832; NID:931166; PIDN:CAA40163.1; PID:931167

A:Note: the nucleotide sequence was submitted to the EMBL Data Library, November 1

C:Genetics:

A:Gene: GDB:ENO3

A:Cross-references: GDB:119873; OMIM:131370

A:Map position: 17pter-17p12

A:Introns: 29/1; 61/1; 80/3; 104/1; 148/3; 223/1; 289/1; 356/2; 392/3; 412/2

C:Superfamily: enolase

C:Keywords: carbon-oxygen lyase; gluconeogenesis; glycolysis; hydro-lyase; muscle;

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

RESULT 15
 J04186
 phosphopyruvate hydratase (EC 4.2.1.11) alpha chain - chicken

N:Alternate names: alpha-2-phospho-D-glycerate hydrolase; enolase

C:Species: Gallus gallus (chicken)

C:Date: 10-Sep-1995 #sequence_revision 27-Oct-1995 #text_change 20-Jun-2000

C:Accession: J04186

R:Tanaka, M.; Maeda, K.; Nakashima, K.

J. Biochem. 117, 554-559, 1995

A:Title: Chicken alpha-enolase but not beta-enolase has a Src-dependent tyrosine-p

A:Reference number: J04186; MUID:95355305

A:Accession: J04186

A:Molecule type: mRNA

A:Residues: 1-434 <TRAN>

A:Cross-references: DDBJ:D37900; NID:974175; PIDN:BA407132.1; PID:974176

A:Experimental source: brain

C:Comment: This is a glycolytic enzyme and multiple isoenzyme forms were reported

rates for tyrosine phosphorylation in Rous sarcoma virus and is important in all t

C:Superfamily: enolase

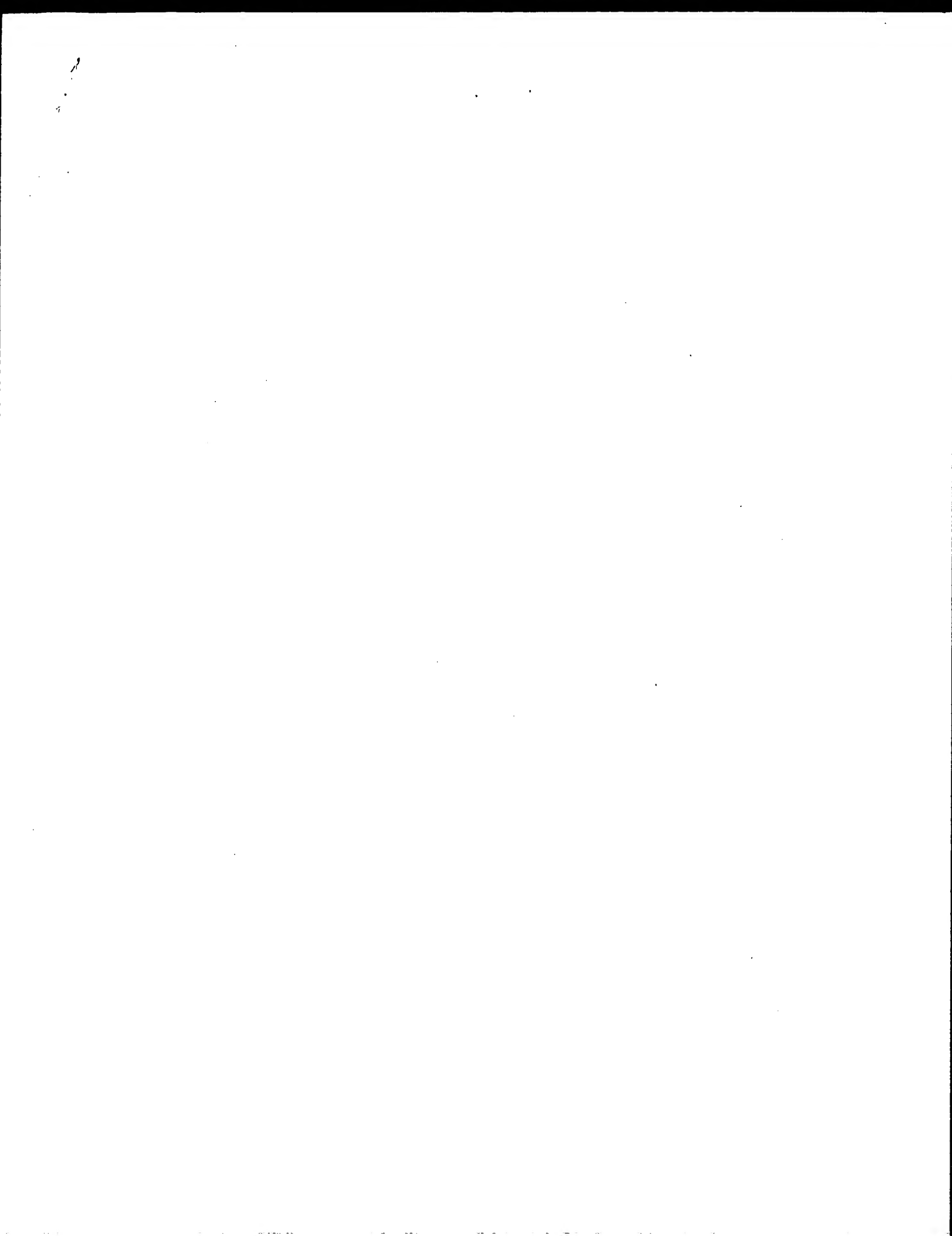
C:Keywords: carbon-oxygen lyase; hydro-lyase; phosphoprotein

F:44/Binding site: phosphate (Tyr) (covalent) #status predicted

Query Match 43.8%; Score 7; DB 2; Length 434;
 Best Local Similarity 100.0%; Pred. No. 3.2;
 Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1 LVVGLCT 7
 |||||
 Db 384 LVVGLCT 390

Search completed: May 8, 2002, 11:47:42
 Job time: 112 sec



GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:43:34 ; Search time 12.53 Seconds

(without alignments)
28.735 Million cell updates/sec

Title: US-09-647-457-2

Perfect score: 90

Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 21252 seqs, 22503292 residues

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued_Patents_AA:*

1: /cgn2_6/ptodata/2/1aa/5A.COMB.pep:*

2: /cgn2_6/ptodata/2/1aa/5B.COMB.pep:*

3: /cgn2_6/ptodata/2/1aa/6A.COMB.pep:*

4: /cgn2_6/ptodata/2/1aa/6B.COMB.pep:*

5: /cgn2_6/ptodata/2/1aa/PTUS.COMB.pep:*

6: /cgn2_6/ptodata/2/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
1	46	51.1	45	1	US-07-973-852-1	Sequence 1, Appl
2	46	51.1	45	1	US-07-950-773-1	Sequence 1, Appl
3	43	47.8	661	1	US-08-232-538-12	Sequence 12, Appl
4	43	47.8	661	2	US-08-786-164-12	Sequence 12, Appl
5	43	47.8	687	1	US-08-232-538-6	Sequence 6, Appl
6	43	47.8	687	2	US-08-786-164-6	Sequence 6, Appl
7	43	47.8	758	2	US-08-874-678-1	Sequence 1, Appl
8	43	47.8	758	3	US-08-643-839-1	Sequence 1, Appl
9	43	47.8	758	4	US-09-051-363-24	Sequence 24, Appl
10	43	47.8	780	1	US-08-232-538-14	Sequence 14, Appl
11	43	47.8	780	2	US-08-786-164-14	Sequence 14, Appl
12	43	47.8	1311	1	US-08-340-011-5	Sequence 5, Appl
13	43	47.8	1311	3	US-08-901-710-5	Sequence 5, Appl
14	43	47.8	1338	2	US-08-750-141A-3	Sequence 3, Appl
15	43	47.8	1362	2	US-08-874-678-3	Sequence 3, Appl
16	43	47.8	1362	3	US-08-643-839-3	Sequence 3, Appl
17	41	45.6	45	2	US-08-824-379-2	Sequence 2, Appl
18	41	45.6	177	2	US-08-465-794-17	Sequence 17, Appl
19	41	45.6	177	3	US-09-049-813-17	Sequence 17, Appl
20	41	45.6	178	2	US-08-465-794-18	Sequence 18, Appl
21	41	45.6	178	3	US-09-049-813-18	Sequence 18, Appl
22	41	45.6	178	4	US-08-663-191A-4	Sequence 4, Appl
23	40.5	45.0	2556	1	US-08-185-432-17	Sequence 17, Appl
24	40.5	45.0	2556	1	US-08-083-590A-20	Sequence 20, Appl
25	40.5	45.0	2556	3	US-08-532-384-20	Sequence 20, Appl
26	39.5	43.9	2523	1	US-08-185-432-18	Sequence 18, Appl
27	39	43.3	95	4	US-09-177-249-273	Sequence 273, App

28	39	43.3	481	1	US-07-927-071-1	Sequence 1, Appl
29	39	43.3	481	6	5164481-1	Patent No. 5164481
30	39	43.3	689	4	US-09-177-249-2	Sequence 2, Appl
31	39	43.3	689	4	US-09-061-769A-2	Sequence 1, Appl
32	39	43.3	992	1	US-08-127-459A-1	Sequence 1, Appl
33	39	43.3	992	1	US-08-482-847-1	Sequence 3, Appl
34	39	43.3	1063	1	US-08-093-453B-3	Sequence 8, Appl
35	39	43.3	1063	1	US-08-127-459A-8	Sequence 8, Appl
36	39	43.3	1063	1	US-08-482-847-8	Sequence 8, Appl
37	38.5	42.8	615	6	5172197-51	Patent No. 5172197
38	38.5	42.8	410	6	5177197-1	Patent No. 5177197
39	38.5	42.8	1394	6	5177197-30	Patent No. 5177197
40	38	42.2	37	2	US-08-248-839C-65	Sequence 65, Appl
41	38	42.2	45	2	US-08-824-379-3	Sequence 3, Appl
42	38	42.2	307	4	US-09-049-672A-9	Sequence 9, Appl
43	38	42.2	461	1	US-08-385-228-2	Sequence 2, Appl
44	38	42.2	461	2	US-08-650-000-2	Sequence 2, Appl
45	38	42.2	461	4	US-08-476-862-2	Sequence 2, Appl

ALIGNMENTS

RESULT 1
US-07-973-852-1
; Sequence 1, Application US/07973852
; Patent No. 5376640
; GENERAL INFORMATION:
; APPLICANT: Miyazaki, Toshiyuki
; APPLICANT: Motoi, Hirofumi
; APPLICANT: Kodama, Toshiaki
; APPLICANT: Maeda, Tatsuhiro
; APPLICANT: Tsujita, Takahiro
; APPLICANT: Okuda, Hiromichi
; TITLE OF INVENTION: LIPOLYTIC ENZYME INHIBITORS
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MATER & NEUSTADT,
; STREET: 1755 Jefferson Davis Highway, Fourth Floor
; CITY: Arlington
; STATE: Virginia
; COUNTRY: U.S.A.
; ZIP: 22202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/973,852
; FILING DATE:
; CLASSIFICATION: 530
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 07/631,321
; FILING DATE: 20-DEC-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 332884/1989
; FILING DATE: 25-DEC-1989
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 75600/1990
; FILING DATE: 27-MAR-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: JP 194782/1990
; FILING DATE: 25-JUL-1990
; ATTORNEY/AGENT INFORMATION:
; NAME: Oblon, No. 5376640man F.
; REGISTRATION NUMBER: 24,618
; REFERENCE/DOCKET NUMBER: 1327-014-0 DIV
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (703)521-4500
; TELEFAX: (703)486-2347
; TELEX: 248855 OPAT UR

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,164
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mark Hand, J
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18888DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 661 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-786-164-12

Query Match 47.8%; Score 43; DB 2; Length 661;
Best Local Similarity 50.0%; Pred. No. 89;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGPA 15
|||:::|
DB 281 GLYTCRVRSGPS 292

RESULT 5
US-08-232-538-6
Sequence 6, Application US/08232538
Patent No. 5712380
GENERAL INFORMATION:
APPLICANT: Thomas, Kenneth A.
APPLICANT: Kendall, Richard L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
TITLE OF INVENTION: GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000 126 E Lincoln Avenue
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0907
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/232,538
FILING DATE:
CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Wallen, John W.III
REGISTRATION NUMBER: 35,403
REFERENCE/DOCKET NUMBER: 188881A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (908) 594-3905
TELEFAX: (908) 594-4720
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:

LENGTH: 687 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-232-538-6

Query Match 47.8%; Score 43; DB 1; Length 687;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGPA 15
|||:::|
DB 307 GLYTCRVRSGPS 318

RESULT 6
US-08-786-164-6
Sequence 6, Application US/08786164
Patent No. 5861484
GENERAL INFORMATION:
APPLICANT: THOMAS, KENNETH A.
APPLICANT: KENDALL, RICHARD L.
TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
TITLE OF INVENTION: CELL GROWTH FACTOR
NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: Merck & Co., Inc.
STREET: P.O. Box 2000, 126 E. Lincoln Ave.
CITY: Rahway
STATE: NJ
COUNTRY: USA
ZIP: 07065-0900
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Microsoft Word 6.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/786,164
FILING DATE: 21-JAN-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mark Hand, J
REGISTRATION NUMBER: 36,545
REFERENCE/DOCKET NUMBER: 18888DA
TELECOMMUNICATION INFORMATION:
TELEPHONE: 908-594-3905
TELEFAX: 908-594-4720
TELEX:
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 687 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-786-164-6

Query Match 47.8%; Score 43; DB 2; Length 687;
Best Local Similarity 50.0%; Pred. No. 92;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGPA 15
|||:::|
DB 307 GLYTCRVRSGPS 318

RESULT 7
US-08-874-678-1
; Sequence 1, Application US/08874678
; Patent No. 5952199
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonard
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
; TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
; STREET: Four Embarcadero Center, Suite 3400
; CITY: San Francisco
; STATE: California
; COUNTRY: United States
; ZIP: 94111-4187
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/874,678
; FILING DATE: HEREWITH
; CLASSIFICATION: 435
; PRIORITY APPLICATION DATA:
; APPLICATION NUMBER: US 08/643,839
; FILING DATE: 07-MAY-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Dreger, Walter H.
; REGISTRATION NUMBER: 24,190
; REFERENCE/DOCKET NUMBER: A-63291-1/WHD
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (415) 781-1989
; TELEFAX: (415) 398-3249
; TELEX: 910 277299
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 758 amino acids
; TYPE: amino acid
; STRANDEDNESS: unknown
; TOPOLOGY: unknown
; MOLECULE TYPE: protein
US-08-874-678-1

Query Match 47.8%; Score 43; DB 2; Length 758;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGA 15
|||:::|
DB 307 GLYTCRVRSGPS 318

RESULT 8
US-08-643-839-1
; Sequence 1, Application US/08643839
; Patent No. 6100071
; GENERAL INFORMATION:
; APPLICANT: Davis-Smyth, Terri L.
; APPLICANT: Chen, Helen H.
; APPLICANT: Presta, Leonard
; APPLICANT: Ferrara, Napoleone
; TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: GROWTH FACTOR ACTIVITY, THEIR USES AND PROCESSES FOR THEIR
; NUMBER OF SEQUENCES: 48
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert

STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/643,839
FILING DATE: 07-MAY-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63291/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 781-1989
TELEFAX: (415) 398-3249
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-643-839-1

Query Match 47.8%; Score 43; DB 3; Length 758;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

OY 4 GLCTCQIKTGA 15
|||:::|
DB 307 GLYTCRVRSGPS 318

RESULT 9
US-09-051-363-24
; Sequence 24, Application US/09051363
; Patent No. 6270993
; GENERAL INFORMATION:
; APPLICANT: Shibuya, Masabumi
; APPLICANT: Okamoto, Masaji
; APPLICANT: Niwa, Makio
; APPLICANT: Matsumoto, Tomoe
; APPLICANT: Asano, Makoto
; APPLICANT: Segawa, Toshiaki
; TITLE OF INVENTION: VEGF-BINDING POLYPEPTIDES
; NUMBER OF SEQUENCES: 24
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/051,363
; FILING DATE: 07-APR-1998
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: PCT/JP96/02906
; FILING DATE: 07-OCT-1996
; APPLICATION NUMBER: 8/211892 JP

FILED DATE: 23-JUL-1996
APPLICATION NUMBER: 7/296476 JP
FILING DATE: 07-OCT-1995
ATTORNEY/AGENT INFORMATION:
NAME: Fraser, Ph.D., J.D., Janis K.
REGISTRATION NUMBER: 34,819
REFERENCE/DOCKET NUMBER: 06501/012001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617/542-5070
TELEFAX: 617/542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 758 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
FRAGMENT TYPE: internal
US-09-051-363-24

Query Match 47.8%; Score 43; DB 4; Length 758;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
|||:::|:
Db 307 GLYTCRVRSGPS 318

RESULT 10
US-08-232-538-14
; Sequence 14, Application US/08232538
; Patent No. 5712380
; GENERAL INFORMATION:
; APPLICANT: Thomas, Kenneth A.
; TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL CELL
; TITLE OF INVENTION: GROWTH FACTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000 126 E. Lincoln Avenue
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0907
; COMPUTER READABLE FORM:
; MEDIUM TYPE: floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/232,538
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Wallen, John W. III
; REGISTRATION NUMBER: 35,403
; REFERENCE/DOCKET NUMBER: 188881A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (908) 594-3905
; TELEFAX: (908) 594-4720
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-232-538-14

Query Match 47.8%; Score 43; DB 1; Length 780;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;
QY 4 GLCTCQIKTGPA 15
|||:::|:
Db 307 GLYTCRVRSGPS 318

RESULT 11
US-08-786-164-14
; Sequence 14, Application US/08786164
; Patent No. 5861484
; GENERAL INFORMATION:
; APPLICANT: THOMAS, KENNETH A.
; APPLICANT: KENDALL, RICHARD L.
; TITLE OF INVENTION: INHIBITOR OF VASCULAR ENDOTHELIAL
; TITLE OF INVENTION: CELL GROWTH FACTOR
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Merck & Co., Inc.
; STREET: P.O. Box 2000, 126 E. Lincoln Ave.
; CITY: Rahway
; STATE: NJ
; COUNTRY: USA
; ZIP: 07065-0900
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: Microsoft Word 6.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/786,164
; FILING DATE: 21-JAN-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER:
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Mark Hand, J
; REGISTRATION NUMBER: 36,545
; REFERENCE/DOCKET NUMBER: 18888DA
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 908-594-3905
; TELEFAX: 908-594-4720
; TELEX:
; INFORMATION FOR SEQ ID NO: 14:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 780 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-786-164-14

Query Match 47.8%; Score 43; DB 2; Length 780;
Best Local Similarity 50.0%; Pred. No. 1e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
|||:::|:
Db 307 GLYTCRVRSGPS 318

RESULT 12
US-08-340-011-5
; Sequence 5, Application US/08340011
; Patent No. 5776755
; GENERAL INFORMATION:
; APPLICANT: Altalo, et al.
; TITLE OF INVENTION: FLT4, A NOVEL RECEPTOR TYROSIN KINASE
; NUMBER OF SEQUENCES: 20

;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
;; STREET: 6300 Sears Tower, 233 South Wacker Drive
;; CITY: Chicago
;; STATE: Illinois
;; COUNTRY: United States of America
;; ZIP: 60606-6402
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: PatentIn Release #1.0, Version #1.25
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/340,011
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/959,951
;; FILING DATE: 09-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Meyers, Thomas C.
;; REGISTRATION NUMBER: 36,989
;; REFERENCE/DOCKET NUMBER: 32267
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1311 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-340-011-5

Query Match 47.8%; Score 43; DB 1; Length 1311;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGA 15
DB 317 GLYTCRVRSGPS 328

RESULT 13
US-08-901-710-5
; Sequence 5, Application US/08901710
; Patent No. 6107046
; GENERAL INFORMATION:
; APPLICANT: Alltalo, Karl
; APPLICANT: Aprelikova, Olga
; APPLICANT: Pajusola, Katri
; APPLICANT: Armstrong, Elna
; APPLICANT: Korhonen, Jaana
; APPLICANT: Kaipainen, Arja
; APPLICANT: Matikainen, Marja-Terttu
; TITLE OF INVENTION: FLT-4, A RECEPTOR TYROSINE KINASE, AND USES
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Marshall, O'Toole, Gerstein, Murray & Borun
; STREET: 6300 Sears Tower, 233 South Wacker Drive
; CITY: Chicago
; STATE: Illinois
; COUNTRY: United States of America
; ZIP: 60606-6402
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25

;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/08/901,710
;; FILING DATE:
;; CLASSIFICATION: 435
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/340,011
;; FILING DATE: 14-NOV-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/257,754
;; FILING DATE: 09-JUL-1994
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 07/959,951
;; FILING DATE: 09-OCT-1992
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Gass, David A.
;; REGISTRATION NUMBER: 38,153
;; REFERENCE/DOCKET NUMBER: 28113/33824
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 312/474-6300
;; TELEFAX: 312/474-0448
;; TELEX: 25-3856
;; INFORMATION FOR SEQ ID NO: 5:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 1311 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: peptide
;; US-08-901-710-5

Query Match 47.8%; Score 43; DB 3; Length 1311;
Best Local Similarity 50.0%; Pred. No. 1.6e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGA 15
DB 317 GLYTCRVRSGPS 328

RESULT 14
US-08-750-141A-3
; Sequence 3, Application US/08750141A
; Patent No. 6011003
; GENERAL INFORMATION:
; APPLICANT: Charnock-Jones, David S.
; APPLICANT: Boocock, Christine A.
; APPLICANT: Smarkey, Andrew M.
; TITLE OF INVENTION: FLT-4-(FMS-LIKE TYROSINE-KINASE),
; TITLE OF INVENTION: FLT-15, VARIANTS THEREOF USED AS GROWTH FACTOR INHIBITORS
; NUMBER OF SEQUENCES: 17
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue, 4th Floor
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/750,141A
; FILING DATE: 12-MAY-1997
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 1396-1-001
; TELECOMMUNICATION INFORMATION:

TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1338 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
HYPOTHETICAL: NO
US-08-750-141A-3

Query Match 47.8%; Score 43; DB 3; Length 1338;
Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
|||:::|:
Db 307 GLYTCRVRSGPS 318

RESULT 15
US-08-874-678-33
Sequence 33, Application US/08874678
Patent No. 5952199
GENERAL INFORMATION:
APPLICANT: Davis-Smyth, Terri L.
APPLICANT: Chen, Helen H.
APPLICANT: Presta, Leonard
APPLICANT: Ferrara, Napoleone
TITLE OF INVENTION: NOVEL INHIBITORS OF VASCULAR ENDOTHELIAL GROWTH FACTOR
TITLE OF INVENTION: ACTIVITY, THEIR USES AND PROCESSES FOR THEIR PRODUCTION
NUMBER OF SEQUENCES: 48
CORRESPONDENCE ADDRESS:
ADDRESSEE: Flehr, Hohbach, Test, Albritton & Herbert
STREET: Four Embarcadero Center, Suite 3400
CITY: San Francisco
STATE: California
COUNTRY: United States
ZIP: 94111-4187
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/874,678
FILING DATE: HEREWITH
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/643,839
FILING DATE: 07-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Dreger, Walter H.
REGISTRATION NUMBER: 24,190
REFERENCE/DOCKET NUMBER: A-63291-1/WHD
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 398-3249
TELEFAX: (415) 781-1989
TELEX: 910 277299
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:
LENGTH: 1362 amino acids
TYPE: amino acid
STRANDEDNESS: unknown
TOPOLOGY: unknown
MOLECULE TYPE: protein
US-08-874-678-33

Query Match 47.8%; Score 43; DB 2; Length 1362;

Best Local Similarity 50.0%; Pred. No. 1.7e+02;
Matches 6; Conservative 5; Mismatches 1; Indels 0; Gaps 0;

QY 4 GLCTCQIKTGPA 15
|||:::|:
Db 305 GLYTCRVRSGPS 316

Search completed: May 8, 2002, 11:45:27
Job time: 113 sec

GenCore version 4.5
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OM protein - protein search, using sw model

Run on: May 8, 2002, 11:45:29 ; Search time 12.46 seconds
(without alignments)
28.897 Million cell updates/sec

Title: US-09-647-457-2
Perfect score: 16
Sequence: 1 LVVGLCTCQIKTGPAC 16

Scoring table: OLIGO
Gapop 60.0 , Gapext 60.0

Searched: 212252 seqs, 22503292 residues

Word size: 0

Total number of hits satisfying chosen parameters: 212252

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database:

Issued Patents_AA: *
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4: /cgn2_6/ptodata/2/1aa/5B_COMB.pep: *
5: /cgn2_6/ptodata/2/1aa/PCTUS_COMB.pep: *
6: /cgn2_6/ptodata/2/1aa/Dackitl1es1.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	5	31.2	12	1	US-08-363-475-3
2	5	31.2	20	3	US-08-658-857B-15
3	5	31.2	20	3	US-08-763-226C-15
4	5	31.2	20	4	US-09-307-200-15
5	5	31.2	43	2	US-08-488-161-60
6	5	31.2	43	3	US-09-273-685-60
7	5	31.2	43	5	PCT-US95-11934-60
8	5	31.2	88	3	US-08-513-974B-340
9	5	31.2	149	3	US-08-425-673-5
10	5	31.2	184	1	US-08-907-800A-2
11	5	31.2	215	1	US-08-431-080-22
12	5	31.2	215	2	US-08-938-534-22
13	5	31.2	248	1	US-08-674-168-32
14	5	31.2	248	3	US-08-985-908-11
15	5	31.2	248	3	US-08-852-730-24
16	5	31.2	248	4	US-09-353-133-3
17	5	31.2	248	4	PCT-US95-02455-3
18	5	31.2	288	3	US-09-335-409-18
19	5	31.2	288	3	US-09-335-409-19
20	5	31.2	311	4	US-08-961-083-184
21	5	31.2	326	1	US-09-413-231-8
22	5	31.2	326	1	US-08-293-563-7
23	5	31.2	327	3	US-08-513-974B-372
24	5	31.2	328	3	US-08-513-974B-39
25	5	31.2	328	3	US-08-513-974B-371
26	5	31.2	333	4	US-09-413-231-10
27	5	31.2	369	1	US-07-816-283-8

28	5	31.2	369	1	US-08-417-103-8
29	5	31.2	369	2	US-08-411-859-3
30	5	31.2	369	4	US-08-120-601B-9
31	5	31.2	369	4	US-08-387-707-9
32	5	31.2	385	3	US-08-053-866-2
33	5	31.2	388	1	US-08-087-772A-2
34	5	31.2	400	1	US-07-916-901-6
35	5	31.2	400	1	US-07-783-602C-1
36	5	31.2	400	1	US-08-351-473B-4
37	5	31.2	400	1	US-08-351-473B-5
38	5	31.2	400	4	US-08-450-962-4
39	5	31.2	400	4	US-08-450-962-6
40	5	31.2	405	1	US-08-351-473B-2
41	5	31.2	420	4	US-08-847-065-19
42	5	31.2	423	4	US-09-243-374-6
43	5	31.2	442	6	5310667-6
44	5	31.2	444	1	US-08-476-008-51
45	5	31.2	444	1	US-08-476-008-52

ALIGNMENTS

RESULT 1
US-08-363-475-3
; Sequence 3, Application US/08363475
; Patent No. 5516679
GENERAL INFORMATION:
APPLICANT: Chiang, Shu-Ten
APPLICANT: Burnett Jr., William V.
TITLE OF INVENTION: PENICILLIN V AMIDOHYDROLASE GENE FROM
TITLE OF INVENTION: FUSARIUM OXISPORUM
NUMBER OF SEQUENCES: 30
CORRESPONDENCE ADDRESS:
ADDRESSEE: Thomas R. Savitsky
STREET: P.O. Box 4000
CITY: Princeton
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 08543
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/363,475
FILING DATE: 23-DEC-1994
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Savitsky, Thomas R.
REGISTRATION NUMBER: 31,661
REFERENCE/DOCKET NUMBER: ON-0134
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 252 4956
TELEFAX: (609) 252 4526
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 12 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
FEATURE:
NAME/KEY: Peptide
LOCATION: 8
OTHER INFORMATION: /note="amino acid 8 can be ser or
; OTHER INFORMATION: Lys"
US-08-363-475-3
Query Match 31.2%; Score 5; DB 1; Length 12;

Best Local Similarity 100.0%; Pred. No. 22;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KTGPA 15
11111
Db 3 KTGPA 7

RESULT 2

US-08-658-857B-15
; Sequence 15, Application US/08658857B
; Patent No. 6040435
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 37
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/658,857B
; FILING DATE: May 31, 1996
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/460,464
; FILING DATE: June 2, 1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099
; INFORMATION FOR SEQ ID NO: 15:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 20 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-658-857B-15

Query Match 31.2%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KTGPA 15
11111
Db 12 KTGPA 16

RESULT 3

US-08-763-226C-15
; Sequence 15, Application US/08763226C
; Patent No. 6057291
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla

STATE: CA
COUNTRY: USA
ZIP: 92037
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: Windows95
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/763,226C
FILING DATE: 10-DEC-1996
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/658,857
FILING DATE: 31-MAY-1996
ATTORNEY/AGENT INFORMATION:
NAME: Haile, Lisa A.
REGISTRATION NUMBER: 38,347
REFERENCE/DOCKET NUMBER: 07420/014001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 619/678-5070
TELEFAX: 619/678-5099
INFORMATION FOR SEQ ID NO: 15:
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-763-226C-15

Query Match 31.2%; Score 5; DB 3; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KTGPA 15
11111
Db 12 KTGPA 16

RESULT 4

US-09-307-200-15
; Sequence 15, Application US/09307200
; Patent No. 6297215
; GENERAL INFORMATION:
; APPLICANT: Hancock, Robert E. W.
; TITLE OF INVENTION: ANTIMICROBIAL CATIONIC PEPTIDES
; NUMBER OF SEQUENCES: 39
; CORRESPONDENCE ADDRESSES:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 4225 Executive Square, Suite 1400
; CITY: La Jolla
; STATE: CA
; COUNTRY: USA
; ZIP: 92037
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/307,200
; FILING DATE:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/763,226
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Haile, Lisa A.
; REGISTRATION NUMBER: 38,347
; REFERENCE/DOCKET NUMBER: 07420/014001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 619/678-5070
; TELEFAX: 619/678-5099

INFORMATION FOR SEQ ID NO: 15;
SEQUENCE CHARACTERISTICS:
LENGTH: 20 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-307-200-15

Query Match 31.2%; Score 5; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 33;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 11 KTGPA 15
|||||
Db 12 KTGPA 16

RESULT 5
US-08-488-161-60
Sequence 60, Application US/08488161
Patent No. 5885577

GENERAL INFORMATION:
APPLICANT: Alvarez, Vernon L.
TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,161
FILING DATE: 07-JUN-1995
CLASSIFICATION: 436
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 60;
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-488-161-60

Query Match 31.2%; Score 5; DB 2; Length 43;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
|||||
Db 39 IKTGP 43

RESULT 6
US-09-273-685-60
Sequence 60, Application US/09273685

Patent No. 6015561
GENERAL INFORMATION:
APPLICANT: Alvarez, Vernon L.
TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/273,685
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/488,161
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-176
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNTE

INFORMATION FOR SEQ ID NO: 60;
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-273-685-60

Query Match 31.2%; Score 5; DB 3; Length 43;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
|||||
Db 39 IKTGP 43

RESULT 7
PCT-US95-11934-60
Sequence 60, Application PC/TUS9511934
GENERAL INFORMATION:
APPLICANT: Cytogen Corporation
TITLE OF INVENTION: Antigen Binding Peptides (Ablides) From
NUMBER OF SEQUENCES: 103
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: USA
ZIP: 10036

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:

APPLICATION NUMBER: PCT/US95/11934
FILING DATE: 20-SEP-1995
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Mistrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-196-228
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 60:
SEQUENCE CHARACTERISTICS:
LENGTH: 43 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: peptide
PCT-US95-11934-60

Query Match 31.2%; Score 5; DB 5; Length 43;
Best Local Similarity 100.0%; Pred. No. 62;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
|||||
DB 39 IKTGP 43

RESULT 8
US-08-513-974B-340
Sequence 340, Application US/08513974B
Patent No. 6114139
GENERAL INFORMATION:
APPLICANT: Hinuma, Shuji
APPLICANT: Hosoya, Masaki
APPLICANT: Fujii, Ryo
APPLICANT: Ohtaki, Tetsuya
APPLICANT: Fukusumi, Shoji
APPLICANT: Ohgi, Kazuhiko
TITLE OF INVENTION: G PROTEIN COUPLED RECEPTOR PROTEIN,
TITLE OF INVENTION: PRODUCTION, AND USE THEREOF
NUMBER OF SEQUENCES: 380
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSHMAN, LLP
STREET: 130 Water Street
City: Boston
STATE: MA
COUNTRY: USA
ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/513,974B
FILING DATE: 14-SEP-1995
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/JP95/01599
FILING DATE: 10-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-093989
FILING DATE: 19-AUG-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-057186
FILING DATE: 16-MAR-1995
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-007177
FILING DATE: 20-JAN-1995
PRIOR APPLICATION DATA:

APPLICATION NUMBER: JP 6-326611
FILING DATE: 28-DEC-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-270017
FILING DATE: 02-NOV-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236357
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-236356
FILING DATE: 30-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189274
FILING DATE: 11-AUG-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189273
FILING DATE: 11-AUG-1945
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-189272
FILING DATE: 11-AUG-1994
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S.
REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 45753
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
TELEFAX: 617-523-6440
INFORMATION FOR SEQ ID NO: 340:
SEQUENCE CHARACTERISTICS:
LENGTH: 88 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-08-513-974B-340

Query Match 31.2%; Score 5; DB 3; Length 88;
Best Local Similarity 100.0%; Pred. No. 1.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 3 VGLCT 7
|||||
DB 66 VGLCT 70

RESULT 9
US-08-425-673-5
Sequence 5, Application US/08425673
Patent No. 5508261
GENERAL INFORMATION:
APPLICANT: Moyie, William R.
APPLICANT: Campbell, Robert K.
TITLE OF INVENTION: Analogs of Glycoprotein Hormones Having
TITLE OF INVENTION: Altered Receptor Binding Specificity and Activity and
NUMBER OF SEQUENCES: 12
CORRESPONDENCE ADDRESS:
ADDRESSEE: Richard R. Muccino
STREET: P.O. Box 1267
City: Princeton
STATE: New Jersey
COUNTRY: USA
ZIP: 08551
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/425,673
FILING DATE:
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/717,151
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: Muccino, Richard R.
REGISTRATION NUMBER: 32,538
REFERENCE/DOCKET NUMBER: UMD 1.0-004
TELECOMMUNICATION INFORMATION:
TELEPHONE: (609) 466-3407
TELEFAX: (609) 466-2760
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 149 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-425-673-5

Query Match 31.2%; Score 5; DB 1; Length 149;
Best Local Similarity 100.0%; Pred. No. 1.8e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 8 CQIKT 12
|||||
DB 93 CQIKT 97

RESULT 10

US-08-907-800A-2
Sequence 2, Application US/08907800A

Patent No. 6001646

GENERAL INFORMATION:

APPLICANT: SUN, Tung-tien

TITLE OF INVENTION: METHOD AND VECTOR FOR EXPRESSION AND

TITLE OF INVENTION: ISOLATION OF BIOLOGICALLY ACTIVE MOLECULES IN URINE

NUMBER OF SEQUENCES: 2

-CORRESPONDENCE ADDRESS:

ADDRESSEE: BROWDY AND NEIMARK, P.L.L.C.

STREET: 419 Seventh Street, N.W., Suite 300

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20004

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/907,800A

FILING DATE: 08-AUG-1997

CLASSIFICATION: 800

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/464,961

FILING DATE: 05-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: BROWDY, Roger L.

REGISTRATION NUMBER: 25,618

REFERENCE/DOCKET NUMBER: SUN-9A

TELECOMMUNICATION INFORMATION:

TELEPHONE: 202-628-5197

TELEFAX: 202-37-5528

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 184 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-907-800A-2

Query Match 31.2%; Score 5; DB 3; Length 184;
Best Local Similarity 100.0%; Pred. No. 2.1e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 LVYGL 5
|||||
DB 170 LVYGL 174

RESULT 11

US-08-431-080-22

Sequence 22, Application US/08431080

Patent No. 5698686

GENERAL INFORMATION:

APPLICANT: Gottschling, Daniel E.

APPLICANT: Singer, Miriam S.

TITLE OF INVENTION: Telomerase Compositions and Methods

NUMBER OF SEQUENCES: 32

CORRESPONDENCE ADDRESS:

ADDRESSEE: Arnold, White & Durkee

STREET: P.O. Box 4433

CITY: Houston

STATE: TEXAS

COUNTRY: UNITED STATES OF AMERICA

ZIP: 77210

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/431,080

FILING DATE: Concurrently Herewith

CLASSIFICATION: 514

PRIOR APPLICATION DATA:

APPLICATION NUMBER: SN 08/326,781

FILING DATE: October 20, 1994

CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:

NAME: Parker, David L.

REGISTRATION NUMBER: 32,165

REFERENCE/DOCKET NUMBER: ARCD:155/PAR

TELECOMMUNICATION INFORMATION:

TELEPHONE: (512) 418-3000

TELEFAX: (713) 789-2679

TELEX: 79-0924

INFORMATION FOR SEQ ID NO: 22:

SEQUENCE CHARACTERISTICS:

LENGTH: 215 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

US-08-431-080-22

Query Match 31.2%; Score 5; DB 1; Length 215;
Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 10 IKTGP 14
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DB 38 IKTGP 42

RESULT 12

US-08-938-534-22

Sequence 22, Application US/08938534

Patent No. 5916752

GENERAL INFORMATION:

APPLICANT: Gottschling, Daniel E.

APPLICANT: Singer, Miriam S.

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? TITLE OF INVENTION: Telomerase Compositions and Methods
? NUMBER OF SEQUENCES: 32
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: Arnold, White & Durkee
? STREET: P.O. Box 4433
? CITY: Houston
? STATE: TEXAS
? COUNTRY: UNITED STATES OF AMERICA
? ZIP: 77210
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS/ASCII
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/938,534
? FILING DATE: 26-SEP-1997
? CLASSIFICATION: 536
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: 08/431,080
? FILING DATE:
? APPLICATION NUMBER: SN 08/326,781
? FILING DATE: October 20, 1994
? ATTORNEY/AGENT INFORMATION:
? NAME: Parker, David L.
? REGISTRATION NUMBER: 32,165
? REFERENCE/DOCKET NUMBER: ARCD:155/PAR
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (512) 418-3000
? TELEFAX: (713) 789-2679
? TELETYPE: 79-0924
? INFORMATION FOR SEQ ID NO: 22:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 215 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
?
? US-08-938-534-22
?
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Best Local Similarity 100.0%; Pred. No. 2.4e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 10 IKTGP 14
DB 38 IKTGP 42
?
RESULT 13
? US-08-674-168-32
? Sequence 32, Application US/08674168
? Patent No. 5804414
? GENERAL INFORMATION:
? APPLICANT: MORIYA, Mika
? APPLICANT: MATSUI, Hiroshi
? APPLICANT: YOKOZAKI, Kenzo
? APPLICANT: HIRANO, Seiko
? APPLICANT: HAYAKAWA, Atsushi
? APPLICANT: IZUI, Masako
? APPLICANT: SUGIMOTO, Masakazu
? TITLE OF INVENTION: METHOD OF AMPLIFYING GENE USING
? TITLE OF INVENTION: ARTIFICIAL TRANSPONSON
? NUMBER OF SEQUENCES: 32
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT,
? ADDRESS: P.C.
? STREET: 1755 JEFFERSON DAVIS HIGHWAY, SUITE # 400
? CITY: ARLINGTON
? STATE: VIRGINIA
? COUNTRY: USA
? ZIP: 22202
?
? COMPUTER READABLE FORM:

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? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/674,168
? FILING DATE: 01-JUL-1996
? CLASSIFICATION: 435
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: JP 7-166541
? FILING DATE: 30-JUN-1995
? ATTORNEY/AGENT INFORMATION:
? NAME: OBION, NORMAN F.
? REGISTRATION NUMBER: 24,618
? REFERENCE/DOCKET NUMBER: 10-810-0
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: (703) 413-3000
? TELEFAX: (703) 413-2220
? TELETYPE: 248855 OPAT UR
? INFORMATION FOR SEQ ID NO: 32:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 248 amino acids
? TYPE: amino acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? MOLECULE TYPE: protein
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? US-08-674-168-32
?
Query Match 31.2%; Score 5; DB 1; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 LVVGL 5
DB 238 LVVGL 242
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RESULT 14
? US-08-985-908-11
? Sequence 11, Application US/08985908
? Patent No. 6004773
? GENERAL INFORMATION:
? APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSH
? APPLICANT: MASAYUKI ARAKI, MASAKAZU SUGIMOTO, YASUHIKO YOSHIHARA, AND TSUYOSH
? TITLE OF INVENTION: METHOD FOR PRODUCING L-LYSINE
? NUMBER OF SEQUENCES: 31
? CORRESPONDENCE ADDRESS:
? ADDRESSEE: OBION, SPIVAK, MCCLELLAND, MAIER & NEUSTADT, P.C.
? STREET: 1755 S. JEFFERSON DAVIS HIGHWAY, FOURTH FLOOR
? CITY: ARLINGTON
? STATE: TEXAS
? COUNTRY: USA
? ZIP: 22202
? COMPUTER READABLE FORM:
? MEDIUM TYPE: Floppy disk
? COMPUTER: IBM PC compatible
? OPERATING SYSTEM: PC-DOS/MS-DOS
? SOFTWARE: Patentin Release #1.0, Version #1.30
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/08/985,908
? FILING DATE: 05-DEC-1997
? CLASSIFICATION: 435
? PRIORITY APPLICATION DATA:
? APPLICATION NUMBER: JP 8-325659
? FILING DATE: 05-DEC-1996
? ATTORNEY/AGENT INFORMATION:
? NAME: NORMAN F. OBION
? REGISTRATION NUMBER: 24,618
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 703-413-3000
? TELEFAX: 703-413-2220
? INFORMATION FOR SEQ ID NO: 11:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 248 amino acids

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TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-985-908-11

Query Match 31.2%; Score 5; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGL 5
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Db 238 LVVGL 242

RESULT 15
US-08-852-730-24
Sequence 24, Application US/08852730
Patent No. 6090597
GENERAL INFORMATION:
APPLICANT: SEIKO HIRANO, MASAKAZU SUGIMOTO, EIICHI NAKANO,
APPLICANT: MASAKO IZUT, ATSUSHI HAYAKAWA, YASUHIKO YOSHIMURA, AND TSUYOSHI
APPLICANT: NAKAMATSU
TITLE OF INVENTION: METHOD OF PRODUCING L-LYSINE
NUMBER OF SEQUENCES: 24
CORRESPONDENCE ADDRESS:
ADDRESSEE: OBLON, SPIVAK, MCCLELLAND, MAIER AND NEUSTADT, P.C.
STREET: 1755 S. JEFFERSON DAVIS HIGHWAY
CITY: ARLINGTON
STATE: VA
ZIP: 22026
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/852,730
FILING DATE: 05-07-1997
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-142812
FILING DATE: 05-JUN-1996
ATTORNEY/AGENT INFORMATION:
NAME: NORMAN F. OBLON
REGISTRATION NUMBER: 24,618
TELECOMMUNICATION INFORMATION:
TELEPHONE: 703-413-3000
TELEFAX: 703-413-2220
INFORMATION FOR SEQ ID NO: 24:
SEQUENCE CHARACTERISTICS:
LENGTH: 248 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-852-730-24

Query Match 31.2%; Score 5; DB 3; Length 248;
Best Local Similarity 100.0%; Pred. No. 2.7e+02;
Matches 5; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 LVVGL 5
|||||
Db 238 LVVGL 242

Search completed: May 8, 2002, 11:47:22
Job time: 113 sec

